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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

AUTHORS	SOURCE SOURCE ORGANISM	VERSION VERSION	DEFINITI	RESULT 1 AX467562		C 45		4.		c 39	38		C 35		c 32		0 29	c 27) 2 5 4	23	321	20	18		n 16	14		c :1:	1 9	ю.	7 6	.	- u	N		Result No.	
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Y.	ntae; Streptophy liophyta; eudico s I; Solanales; :	757	WO0218607.		ALIGNMENTS	AC006269	AL732577	AC022281	AF151388	PFMAL4P4	CNS07ECV	HS1100E15	CNS01RGG	AL590287 PFMAL4P1 1	AL136178	AC079621	HSKB152G3	AC117073	VYIVD10	AC104069 AL359832	AL357136	AC105252	AC108052	AF141654	AL627305	AX345250	AX281353	AC087568	AL593856	AR059252	NTT85A	TOBPSAFA	ഹ	AR059249	55	5:	ID	
decovs that alter protein	ta; Embryophyta; Tracheophyta; tyledons; core eudicots; Solanaceae; Nicotiana.			linear PAT 16-JUL-2002		Homo	AL732577 Zebrafish	AC022281 Homo sapi	AF151388 Dermatobi	AL035477 Plasmodiu	AL442663 Human chr	ALO35551 Human DNA	Human	Human	Human	HOMO	AL132982 Human DNA	AC117073 Dictyoste	Plasi	AC104069 Homo sapi	Humar	HOMO OMO		AF141654 Nicotiana AL035475 Plasmodiu	AL627305 Danio rer	AX346470 Sequence	Sequ	AC087568 Pan trogl	Human DN	ARU59252 Sequence X57079 N.svlvestri		ed opped		AR059249 Sequence	Sequenc		cription	

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Locus	AX467562 456 bp DNA linear PAT 16-JUL-2002
DEFINITION	Sequence 1 from Patent WO0218607.
ACCESSION	AX467562
VERSION	AX467562.1 GI:21900757
KEYWORDS	
SOURCE	common tobacco.
ORGANISM	Nicotiana tabacum
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
	Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
REFERENCE	
AUTHORS	Conkling, M.A. and Li, Y.
TITLE	Transgenic plants containing molecular decoys that alter protein

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BASE COUNT
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Conkling, M.A., Mendu, N. and Song, W.
Root cortex specific gene promoter
Patent: US 5837876-A 3 17-NOV-1998;
Location/Qualifiers
1. .1372
                                                                                                                                                                                                                                                                                                                                                 Unknown.
Unclassified.
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       1 (bases 1 to 2010)
Conkling,M.A., Mendu,N. and Song,W.
Root cortex specific gene promoter
Patent: US 5837876-A 1 17-NOV-1998;
                                                   Unknown
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patent

SD 2010 bp US 5837876.

DNA

PAT

29-SEP-1999

Location/Qualifiers

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Sequence 2
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Conkling,M.A., Mendu,N. and Song,W.
Root cortex specific gene promoter
Patent: US 5837876-A 2 17-NOV-1998;
Location/Qualifiers
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D42070.1 GI:575606
D42070.1 GI:575606
Nicotiana sylvestris (library: lambda DASH) DNA, clone KuEG3.
Nicotiana sylvestris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
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Plant Physiol. 108 (3
95357419
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                                                   Submitted (09-NOV-1994) Junichi Obokata, Hokkaido University, Graduate School of Environm. Earth Sci.; kita-ku, Sapporo, Hokkaido 060, Japan (E-mail: jo@cul.hines.hokudai.ac.jp, Tel:011-706-5291, Fax:011-757-5994)
                                                                                              Obokata, J.
Direct Submission
                                                                                                                                                                                               Kubota, T., Yamamoto, Y.Y. and Cloning of a nuclear-encoded
                                                                                                                                                                                                                                                                                                                                              TOBPSAEB
                                                                                                                                           Obokata, J
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                                                                                                                                            N.tobacum
X70902
                                                       Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 6053)
                                                                                                            auxin binding protein; Nicotiana tabacum.
         Shimomura,S.
Direct Submission
Submitted (19-JAN-1993) S.
Agrobiological, Resources,
                                                                                                                                    X70902.1
                                                                                                                                                                   NTT85A
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2018. .2274
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1090. .1397
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Pred. No. 5.9e-28;
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            Shimomura,
Kannondai
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            , National Institute of 2-1-2, Tsukuba, Ibaraki
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279 60

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                                           Local Sim thes 314;
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2 (bases 1 to 6053)
Watanabe,S. and Shimomura,S.
Cloning and expression of two genes encoding auxin-binding proteins
Plant Mol. Biol. 36 (1), 63-74 (1998) 98145457
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                                           h 40.4%; Score 184.2; DB 8; Similarity 74.2%; Pred. No. 5.5e-19; 14; Conservative 0; Mismatches 98;
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/db_xref="GI:20034"
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/cultivar="NK326"
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/gene="T85"
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2748 .3212
/gene-"T85"
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                                                                        Length 6053;
                                               Indels
                                               11; Gaps
                                               6,
    ACCESSION
    N.SYIVESTI15 DNA FOR 31KD Chloropidso
X57079 S38099 S38103 S38111 S38122
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D Qy	Qy Db	Qy дь	Query Best I Matche	BASE COU	TITLE JOURNA FEATURES	REFERENC	SOURCE	DEFINITI ACCESSIC VERSION	RESULT 9 AR059252 LOCUS	Db	Qy	D Qy	Db	Qγ	Db .5	Ov	Qy Db	Db	γQ	DB ·	Qy	Db
429 TIGTTATAGGTAAAAAGCAGTTACAGAG 456 	369 CGGTGCGGACGGTTCGATCGGTTTAGTCGATTTTCAAATATTCA 	309 GTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCAGAAGA 	32.5%; Score 148; DB 6; Le similarity 100.0%; Pred. No. 2.6e-13; Conservative 0; Mismatches 0;	/organism="unknown" COUNT 277 a 108 c 129 g 208 t	HORS CONTING.M.A., Meduc,N. and Sony,W. LE Root cortex specific gene promoter IRNAL Patent: US 5837876-A 6 17-NOV-1998; IRES Location/Qualifiers source 1722	ANISM Unknown. Unclassified. Unclassified. 1 (bases 1 to 722)	RDS Unknown.	Sequence 6 from patent US 5837876. AR059252 AR059252.1 GI:5984829	AR059252 722 bp DNA 11	1462 ATT 1464	428 GTT 430	368 TCGGTGCGGACGGTTCGATCGGTTTAGTCGATTTTCAAATATTCA 						1166 GAGTTTAATTA-TTGTTGACTTGTAACTGTTTTCATAATCCCAAC	132 GAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAG		72 TACTTGAAATAGCTTAGTTTAAATATAAATAGCATAATAGATTTT	1047 AAACATATTTATTTGCTACTCATAATCGCTACAATACCTTGTGTCTTAGCTTGCTAGTTA
	TTGACACTCCTAGTTG 428	AACCTAAAAATCGGTT 368 AACCTAAAAATCGGTT 60	h 722; els 0; Gaps 0;						ear PAT 29-SEP-1999			ATTGACACTCCTAGTT 427 ATCGAAATCCCTACTC 1461	NAATCTAAAAATCGAT 1404	NAACCTAAAAATCGGT 367	<u></u>	STTACCCTAATTATCG 308	PAAAATTTAATCG 248 PATGTAAATTTACTCG 1284	PACCAAGGAAAAATTT 1224	GCCCATGAAAAATTT 191	 3A-GAATTAGGATTTT 1165	RAGGAATTAGTATTTT 131	TTAGCTTGCTAGTTA 1106
	429 TTGTTATAGGTAAAAAGCAGTTACAGAG 45	369 CGGTGCGGACGGTTCGATCGGTTTAGTCGATTTCAAATATTCAATTGACACTCCTAGTTG	309 GTACAGTTATAGATATAAAATCTACGGTTCTTCAGAAGAAACCTAAAAATCGGTT	Query Match 32.5%; Score 148; DB 6; Length 722; Best Local Similarity 100.0%; Pred. No. 2.6e-13; Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 309 GTACAGTTATAGATTATATATAAAATCTACGGTTCTTCAGAAGAAACCTAAAAATCGGTT 36 I GTACAGTTATAGATATATATATAAAAATCTACGATTTTCAAATATTCATTGACACCTCCTAGTTG 369 CGGTGCGGACGGTTCGATCGGTTTAGTCGATTTTCAAATATTCATTGACACCTCCTAGTTG [COUNT 277 a 108 c 129 g 208 t (NO 129 g 148; DB 6; Length 722; (NO 120 g 148; Conservative 0; Mismatches 0; Indels 0; Gaps 16	THORS CORKING, M.A., Mendu, N. and Song, W. TLE Root cortex specific gene promoter IRNAL Patent: US 5837876-A 617-NOV-1998; IRES Location/Qualifiers SOURCE 1.722 COUNT 277 a 108 c 129 g 208 t IN 32.5%; Score 148; DB 6; Length 722; ST Local Similarity 100.0%; Pred. No. 2.6e-13; ST Local Similarity 100.0%; Pred. No. 2.6e-13; The Conservative 0; Mismatches 0; Indels 0; Gaps 148; Conservative 0; Mismatches 0; Indels 0; Gaps 309 GTACAGTTATAGATTTATATATAAAATCTACGGTTCTTCAGAAGAAACCTAAAAATCGGTT 1	NENCE 1 (bases 1 to 722) RENCE 1 (bases 1 to 722) CONKING, M.A., Mendu,N. and Song,W. PHORS CONKING,M.A., Mendu,N. and Song,W. RES CONKING,M.A., Mendu,N. and Song,W. RES RES Location/Qualifiers SOURCE 1.722 COUNT 277 a 108 c 129 g 208 t RENCE 1.325	Unknown. Unknown. Unknown. Unknown. Unclassified. Unclassified. In (bases 1 to 722) 1 (bases 1 to 722) 1 (bases 1 to 722) 1 (coakling,M.A., Mendu,N. and Song,W. Coakling,M.A., Mendu,N. and Song,W. Root cortex specific gene promoter Root cortex specific	Sequence 6 from patent US 5837876. AR059252.1 GI:5984829 . White the content of	AR059252 AR059252 AR059252.1 GI:5984829 Unknown. Unknown. Unclassified. 1 (bases 1 to 722) 1 (bases 1 to 722) 2 Patent: US 5837876.A 6 17-NOV-1998; 3 Conkling,M.A., Mendu,N. and Song,W. Root cortex specific gene promoter Patent: US 5837876.A 6 17-NOV-1998; 4 Conkling,M.A., Mendu,N. and Song,W. Root cortex specific gene promoter Patent: US 5837876.A 6 17-NOV-1998; 5 Conkling,M.A., Mendu,N. and Song,W. Accombined to 722) 1 (bases 1 to 722) 2 (conkling,M.A., Mendu,N. and Song,W. Conkling,M.A., Mendu,N. and Song,W. Conkling,W. Co	AR059252 722 bp DNA linear PAT 29-SEP-19-Sequence 6 from patent US 5837876. AR059252 AR059252.1 GI:5984829 Unknown. Unclassified. 1 (bases 1 to 722) 1 (bases 1 to 722) 2 (conkling, M.A., Mendu, N. and Song, W. Conkling, M.A., Mendu, N. and Song, W. Constitution/Qualifiers 1 722 1	128 GTT 430	168 TCGGTGCGGACGGTTCGATCGGTTTAGTCGATTTCAAATATTCATTGACACTCCTAGTT 42		OF GTACAGTTATAGATTTATATAAAATCTACGGTTCT-TCAGAAGAAACCTAAAATCGGT 36:		49 GTATAGTTGGATATTTTTTCAATTTATATAAAAAACTTAAAACTTAAACTTAATTATG 11	29 AARGCTTTARTAGTTTTAAACTTACTARTATATTTTCATATGA	6.6 GASTITMANTA TIGOTICACTITICATATATATCCCAACCAAGGAAAATT 12: 9.2 AATGCTTTATATATTATATCTTTAAATTATATCCCAACCAA	32 GAGTTTAATTACTTATTACTTGTAACATTTTATAATTCCAAGGCCCATGAAAAATTT 19:		72 PACTTGANATAGGTTAGATTAGATTAGATTTAGGATTAGGATTTAGGATTTAGGATTTAGGATTTAGGATTTAGATTTT 13

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REFERENCE
AUTHORS
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (27-DEC-1990) M. Sugiura, CEN NAGOYA UNIVERSITY, NAGOYA 464-01, JAPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sugiura, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 5040)
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 GGAAACATATTCAATACATTGTAGTTTGCTACTCATAATCGCTAGAATACTTTGTGCCTT 60
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                                 Conservative
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EEEGFVEAVGDAGESDEVEADEEEEEEFQEPPEDAKLFVGNLPYDVDSEGLARLFEQAG
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join(2099. .2596,2830.
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                                                20.7%;
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                                 0
                                                Score 94.4; DB 8; Pred. No. 1.5e-05;
                                 Mismatches 116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human DNA sequence from clone
                                                                                                                                                                                   Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1 RP11-8J9 is from the library RPCI-11.1 constructed by Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    requests: clonerequest@sanger.ac.uk
on Oct 2, 2001 this sequence version replaced g1:15591654.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (03-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chapman,
                           This sequence is the entire insert of clone RP11-8J9 The true left end of clone RP4-732G19 is at 98457 in this sequence. The true right end of clone RP11-49P4 is at 37956 in this sequence.

Location/Qualifiers
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298547.2 GI:15383894
HTG; 608 Acidic ribosomal protein P2; asparagine synthetase; calcium-dependent protein kinase; DNA polymerase delta; dual specificity protein phosphatase; guanine nucleotide-binding protein; PDZ domain; rat BRAIN-like protein; serine/threonine protein; PDZ domain; rat BRAIN-like protein; serine/threonine
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                                                                                                                                                                        Bowman, S., Lawson, D., Basham, D., Brown, D., Chillingworth, T., Churcher, C.M., Craig, A., Davies, R.M., Devlin, K., Feltwell, T., Gentles, S., Gwilliam, R., Hamlin, N., Harris, D., Horroyd, S., Hornsby, T., Horrocks, P., Jagels, K., Jassal, B., Kyes, S., McLean, J., Moule, S., Mungall, K., Murphy, L., Oliver, K., Quail, M.A., Rajandream, M.-A., Rutter, S., Skelton, J., Squares, R., Squares, S., Suston, J.E., Whitehead, S., Woodward, J.R., Newbold, C. and
                                                                                                                                                                                                                                                                                                                                                      protein kinases; T-complex protein eta; T08A11.2-like protein domain; Y48E1C.2-like protein.
Plasmodium falciparum 3D7.
Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 116696)
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/note="Sequence from overlapping clone RP4-732G19 (AL356793). Assembly confirmed by restriction digest." a 32904 c 32733 g 46543 t
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/db_xref="taxon:9606"
/chromosome="1"
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AUTHORS
TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum. The following numbers may have changed slight-3D. The true left end of clone MY434-3D7 is at 1 in this sequence. The true right end of clone MY549-3D7 is at 79511 in this sequence. The true right end of clone MY549-3D7 is at 114736 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CB10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On or before Aug 31, 2001 this sequence version gi:2894463, gi:2894495, gi:2894369, gi:2982521,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mungall, K., Bowman, S., Churcher, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g1:3649752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lawson, D., Bowman, S. and Barrell, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rajandream, M.-A. and Barrell, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="I
6740. .8
                     /note="Match to PF00595 PDZ, PDZ domain (Also known or GLGF). Score 20.36" complement(join(9589. .16129,16327. .20041,20295. ./gene="PFC0335c, MAL3P3.3" .16129,16327. .20041,20295. ./gene="PFC0335c, MAL3P3.3" .20041,20295. ./gene="PFC0335c, MAL3P3.3" hypothetical protein, note="PFC0335c, (MAL3P3.3), hypothetical protein, 3724 aa, predicted using hexexon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="part exon 3 of PFC0235c" complement(4520. .4587) note="exon 2 of PFC0235c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the exons are shown protein id*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"region duplicated in MAL3P2 to include the whole of PFC0235c in one entry, the whole CDS is in MAL3P2 and only the exons are shown in this entry to avoid duplicating the
                                                                                                                                                                                                                                                                                                                                                                                            KRICVSYNMKSHTFKRSISNLSDLIEFSNKLKYVLDERIHKLYYEDKNNENÄYLNKTL
RKELEIGKKERDYTNLSKKNLOMSIESSLKLIEKCMONMYKONYEITLHDLKLAYNML
PCKYYGFFLSNLCSTISTLSYYVNDLOGTFNFALKSIKYEPKYNVAMKCLGDAYRSFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6740.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(4804. .4830)
/note="exon 1 of prc0235c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(1. .4302)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Plasmodium falciparum/strain="3D7"
                                                                                                                                                                                                                                                                                                                KFWQAKNFYDIAIYLGYKDEKGERFEDIVQELNNLTENALKNYDLLKEHMNNSTNIII
KKNIGIVLNKNPDSIGGCYVSYIIEGSKASKKNLHHGDQIVALNNHVTYGKPIDFCLK
AFQKNDGTYDIIFFKGNIIELYGLKAYKYLMKNDLFYALFENEQIVSFKRNETILFDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNPTNNS IDNPTNNS IDNPTNNS IDNPTNNSTDNP INSPNYQQVTQSNI I LEEENNTN
KTD I EKD I IN INFYSSEEKK I ACEM I KDQ I YYLLHSSMDKT FIETFNI NI ESH I VPSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="putative PDZ domain
/protein_id="CAB11102.1"
/db_xref="GI:3649753"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as DHR or GLGF). Score 20.36, predicted using hexExon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:36329"
/chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KQRINSKHYTFLYKNDTLNKLLNRKKNKHTLFYRSKKEKDIQESGYLYPFDHLEKKKT
KFPPDPYIPSEDEKESSIDIFHDKINDDDLMIYEDDDDAKKYFGKTTFNKPNIIQKDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="PFC0330w, MAL3P3.2"
/note="PFC0330w (MAL3P3.2), putative PDZ domain protein,
len: 700 aa, Match to PF00595 PDZ, PDZ domain (Also know
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone-"MAL3P3"
                                                                                                                                                                                                                                    /gene="PFC0330w, MAL3P3.2"
                                                                                                                                                                                                                                                                                           KGFGTFSEYGMSKAEFV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NSEDDQDDDLNDQNDDP I NNPT NNLTDNPT NNST DNPT NNS I DNPT NNS I DNPT NNS I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MYLLMSKFLVWIIIFGNEFVVHFFLCFKIPNNKITNVLTYDNSk/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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                                                                                                                                                                                                            PDZ domain (Also known
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/product="hypothetical protein,
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NNNNNNNNNNDNNINVGYKRMQNNINPNNLYEIKNNNFNLYHRYWSLFYKYCPVSYI
NDNKIIEGKKKFCVIYKNKIYMLNNHDYMIEFLKHPKFYASKKVKESVCFSLVIYFPN
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ENFLIISYMNEEIYFLIKKLKVEIIEPSIILNKNMHIEKQFLSPLGKYINDNLKEGKC
ISSKIIIDLMLEYMNTIISKNNGYVLYFNNYNILQHLDYFLHKLKGLSTIKYINYVHF
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ILYDENQVYSVLYSDHKIEQDIQDIHSIQTNICDENNIEQINEENSKKGVRISGTDME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VETNEKQRKKTNKKKSVQKDDLVEENALLDNLIIIDGINFDDVTKECKIIDDNNNENI
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I PPLRLLFLYDVPYKFNKD I KKNMYRKFFFKY I NLEKEC I IY I KYVF IYLLKY I FLFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>ERESRORYIITGLPLHSKIFFYLKCMNISIDHVISFDIIKKEMNKDEENEDKGDGDDF</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKKKNILINQCEIKKKMKRKKKMKKKKKKKIPEKKKLVNNEKKNLLFLFSSIMKIKFL
YNLIIIKQKNIKNVSFKNVLDKLSHIINIKDMAKDINLLLVLIEDMFFREKRKYLNKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DAHIFEIHRIIEGKTISPLFIVRYICIHMKKIHQFNIYIIKEIIKSIIKLKHNFNLLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KYCDDMEHEKDLSMLIKHLSVLLKDEKENIKNNEGGEESIDNILIDKNMKSDQEYNEN
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                                                                                                                                                             YINLYDKILYSQTITNKTKOKKIKYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIFVYSCIEIENLHNELHKSTKCVVINREHLLSFGNKIKKYEKYIQTNNIDDNILMEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YIDIEKYHSKSIKMLIEKRLNDILRYRQNLYHQLNMKRIDKICAQFLRDNNYIKFSNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLKYAFRVPEYVIYLGCTSPKKLLDRMKKVKNVEQIKNSEHTNHVTNSKGDGRKNPND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IYKYDYKKKTNIDIKNFSINSIPIKNLLEKKYIYYLYREDIIYLENNINQINVYEQNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   I I NNY NDKC I T NDMNVKQNVNHNNI NS PNDKDNI HMI NDEY KKKKY I NTSFTLLSKKK
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                                                                        23110. .24606
/gene="PFC0340w, MAL3P3.4"
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gene Sg

ORGANISM

Pan troglodytes

troglodytes.

Pan troglodytes clone RP43-135M11, AC087568

150199 bp

complete sequence.

linear

PRI 02-NOV-2001

GI:16596569

AC087568.2

AC087568

AUTHORS

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brook Blakesley,R.W., Gunta,X., Guta,J., Haghighi,P., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Ho,S.-L., Idol,J.R., Karlins,E., Laric,P., Lee-Lin,S.-Q., Legaspi,R., Maduro,Q.L., Maduro,V.B., Masiello,C., Mastrian

Mastrian, S.D.,

Brooks, S.,

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. 1 (bases 1 to 150199).

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Matches 183;
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71903 TTTATTTAATTATATTGTTATCATTCAATGGACTATATATTTTTTAAAAACTAAAA 71848
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                                                                                                                 TCGGTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCAGAAGAAACCTAAAA 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="Sptrembl:077321"
/db_xref="Sptrembl:077321"
/translatioo="mdekvtnoeveelikhinenkknegehonkkikkkhfeyvnise
R/tianslatioo="mdekvtnoeveelikhinenkknegehonkkikkninndninnd
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YSKNNKMNALKLIAQSRILSPTSPDTLGCYPFTKNDPFCLNDDNTYPHIFINGNCSKL
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25880. .31015
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LRNFILRLHGDTYLSENLIRLIILGNSLSNIDNDEKDMNTIDVFLSSLCSSIHIDLMP
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/protein_id="CAB11105.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McCloskey,J.C., McDowell,J., Pearson,R., Prasad,A., Shevchenko,Y., Stantripop,S., Thomas,J.W., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLONE LENGIH: This sequence represents the entire insert of this clone unless otherwise noted. If there are overlapping clones, the overlaps are noted in the beginning and end of
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Similarity 48.7%;
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GCGGACGGTTCGATCGGTTTAGTCGATTTTCAAATATTCATTGACACTCCTAGTTGTTGT 432
                                              TAATAAAACTATATAAATATTTTATATTTATATTAATCTATATAAATTATATTTATAT 38988
                                                                                                                                                                                             AGTTCGATATTTTTCAATTTATTTTTATAAAATAAAAAACTTACCCTAATTATCGGTAC 312
                                                                                                                                                                                                                                                ATGCTTTATTAGTTTTAAACTTACTATATAAATTTTTCATATGTAAAATTTAATCGGTAT 252
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                                                                                              AGTTATAGATTTATATAAAAAATCTACGGTTCTTCAGAAGAAACCTAAAAATCGGTTCGGT 372
                                                                                                                                                 ATATAAATATATTTTATATTATATTAATAAAAACTATATAAAATATATTTTATATTTATAT 38928
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Contact: nisc_mouse@nhgri.nih.gov
-------- Project Information
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Center clone name: 135M11
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/db_xref="taxon:9598"
/clone="RP43-135M11"
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36322 c 37037 g 40339 t
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Sequence 321 from Patent
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Olek, A., Piepenbrock, C. and Berlin, K. Diagnosis of diseases associated with
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/db_xref="taxon:32630"
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Search completed: June 9, 2003, 07:42:26
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Best Local Similarity 51.9%;
Matches 176; Conservative
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                                                                  747 TGTTTATATTATGATTTAATTAATTTTTTTTTTTTTAGATATTTAAATTGTTTTAA 806
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/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
/note="chemically treated genomic DNA (Homo sapiens)"
/note="chemically treated genomic DNA (Homo sapiens)"
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12.4	12.4	12.4	12.4	12.4	12.4	12.5	12.5	12.5	12.5	12.5	12.5	12.6	12.6	12.6	12.6	12.6	12.6	12.7	12.7	12.7	12.8	12.8	12.8	12.8	12.9	13.0	13.1	13.2	13.2	13.2	13.2	13.2	13.2	13.4	14.6	
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ABL34475	ABL32361	ABL70150	AAS46310	ABK31361	AAS61265	ABL17264	ABK40038	ABL70376	ABL34135	ABK33986	AAS46479	AAD22328	ABL33591	ABL92277	ABL34129	ABK33937	AAS46792	ABL34515	ABL70542	AAS61094	AAS63335	ABL33449	AAH93026	AAL15924	ABV10021	AAC58017	ABL34091	ABK69933	AAK73165	ABL33569	ABL33576	ABL32570	ABK33948	ABL33307	ABL33568	
Human metastasis a	Human immune syste	Chemically treated	Tumour suppressor	Signal transductio	Human gene regulat	Drosophila melanog	Human chemically p	Chemically treated	Human immune syste	Human DNA for stag	Tumour suppressor	Chemically treated	Human immune syste	Chemically treated	Human immune syste	Human DNA for stag	Tumour suppressor	Human metastasis a		Human gene regulat	Chemically pretrea	Human immune syste			Human prostate exp	Arachidonic acid m	Human immune syste	Ξ.	Human immune/haema	Human immune syste	Human immune syste	1mmune	Human DNA for stag	immune syst	Human immune syste	

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ALIGNMENTS

RESULT 1 ABL58286 THE STANK CONTRACTOR OF THE ST N. tabacum Nic gene product responsive element DNA sequence. 07-MAR-2002. Tobacco; plant; cis-acting element; transgenic; nicotine; Nic; NtQPT1; nitrosamine; responsive element; ds 15-JUL-2002 ABL58286; ABL58286 standard; DNA; 456 BP. Conkling MA, (UYNC-) UNIV NORTH CAROLINA STATE. 30-AUG-2000; 2000US-229198P 28-AUG-2001; 2001WO-US26788. WO200218607-A2 Nicotiana tabacum. (first entry) Li Y;

Human metastasis

Obtaining plant with altered levels of desired protein regulated cis-acting element by introducing nucleic acid with the element operably linked to coding sequence of the protein to produce a

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WPI; 2002-371827/40.

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AAT5172
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Best Local Similarity
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                                                                                                                                                              Root cortex specific gene TobRD2 promoter (del1.0).
                                                                                                                                                                                                      15-OCT-1997
                                                                                                                                                                                                                                                                                      AAT51750
                       WO9705261-A1
                                                             Nicotiana tabacum
                                                                                                   Root cortex-specific |
Insecticide; Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAAACATATTCAATACATTGTAGTTTGCTACTCATAATCGCTAGAATACTTTGTGCCTT
                                                                                                                                                                                                                                                                                      standard; DNA; 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATCGGTTCGGTGCGGACGGTTCGATCGGTTTAGTCGATTTTCAAAATATTCATTGACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATTATCGGTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCAGAAGAAACCTAAA 360
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                                                                                                                                                                                                                                                                                                                                                                                                                             CCTAGTTGTTATAGGTAAAAAGCAGTTACAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48; 48pp;
                                                                                                                      promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 456; DB 24; 100.0%; Pred. No. 4.3e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; 57 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 G;
                                                                                                                      TobRD2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 T; 0 other;
                                                                                                2; tobacco;
biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 24;
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                                                                                                   control; ss
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RESULT 3
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Query Match
Best Local S
Matches 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1030 BP; 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conkling MA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             directing heterologous gene expression in the root cortex - used . for expressing insecticidal Bacillus proteins
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CCTAGTTGTTGTTATAGGTAAAAAGCAGTTACAGAG
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                                                                                                                                                                                                                                                                                                                             ATGAAAAATTTAATGCTTTAGTAGTTTTAAACTTACTATATAAATTTTTCATATGTAAAA 240
                                                                                                                                                                                                                                                                                                                                                                                                       ATTAGTATTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTAATAAAGATACTTGAAATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGA 120
                                                                                                                                                                       AATTATCGGTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCAGAAGAAACCTAAA
                                                                                                                                                                                                                                                  GCTAATAAAGATACTTGAAATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGA
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                                                                                                                                                      AATTATCGGTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCAGAAGAAACCTAAA
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Pred. No. 4e-68;
Mismatches
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                                       456
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AAT51749 standard; DNA;

1294

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AAT51749;

15-OCT-1997

(first entry)

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Best Local Similarity
Matches 456; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             associated genes. Dell.3 can be used in DNA cassettes to direct the expression of heterologous genes in the root cortex layer of transgenic monocot or dicot plants, e.g. Bacillus thursgiensis crystal proteins in tobacco for the control of root-damaging pests Dell.3 conferred high levels of GUS reporter gene expression (several-fold higher than the CaMV35S promoter) in transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       An isolated DNA (AAT51749), designated del1.3, comprises a 1294 by 5'-deletion mutant of the tobacco RD2 gene (TobRD2) promoter (see also AAT51746), which directs root cortex-specific expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA directing heterologous gene expression in the root cortex - used e.g. for expressing insecticidal Bacillus proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYNC-) UNIV
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                                                                                                                                                            445
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       361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   root cortex.
                                                                                                                                                                                                                                         ATTAGTATTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCC 180
                                                     AATTATCGGTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCAGAAGAAACCTAAA
                                                                                                                TTTAATCGGTATAGTTCGATATTTTTCAATTTTTTTATAAAATAAAAAACTTACCCT 300
                                                                                                                                                                            ATGAAAAATTTAATGCTTTATTAGTTTTAAACTTACTATATAAATTTTTCATATGTAAAA
                                                                                                                                                                                                                                                                                    GCTAATAAAGATACTTGAAATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGA
                                                                                                                                                                                                                                                                                                                  GCTAATAAAGATACTTGAAATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGA 120
                                                                                                                                                                                                                                                                                                                                                GGAAACATATTCAATACATTGTAGTTTGCTACTCATAATCGCTAGAATACTTTGTGCCTT
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       AATCGGTTCGGTGCGGACGGTTCGATCGGTTTAGTCGATTTTCAAATATTCATTGACACT 420
                                                                                                                                                              ATGAAAATTTAATGCTTTATTAGTTTTAAACTTACTATATAAATTTTTCATATGTAAAA
                                                                                                                                                                                                                          ATTAGTATTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            specific promoter; TobRD2; tobacco; transgenic plant;
Bacillus thuringiensis; biological control; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mendu N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96WO-US12158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      designated dell.3, comprises a 1294 bp
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 456; DB 18;
Pred. No. 4e-68;
                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        promoter (del1.3).
                                                                                                                                                                                                                                                                                                                                                                                                           0;
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT51748
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                                                                                                                                                                                                                                                                                     Sequence 1372 BP; 532 A; 187 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 35; 53pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   insecticide;
                                                                                                                                                                                                                                                 Local Similarity
                                                                            463
                                                 181
                                                                                                                              403
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                                                                                                                                            GCTAATAAAGATACTTGAAATAGCTTAGTTTAAATATAATAGCATAATAGATTTTAGGA
                                                                                                                                                                                                GGAAACATATTCAATACATTGTAGTTTGCTACTCATAATCGCTAGAATACTTTTGTGCCTT
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 ATTAGTATTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCC
                                                                                                                                                                                 GGAAACATATTCAATACATTGTAGTTTGCTACTCATAATCGCTAGAATACTTTGTGCCTT
                                                                            ATTAGTATTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCC
                                                                                                                              GCTAATAAAGATACTTGAAATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGA
                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                cortex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NORTH CAROLINA STATE
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                                                                                                                                                                                                                                  100.0%; s
100.0%; F
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thuringiensis;
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                                                                                                                                                                                                                                   Score 456; DB 18;
Pred. No. 3.9e-68;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TobRD2; tobacco; transgenic plant;
ensis; biological control; ss.
                                                                                                                                                                                                                                                                                      215 G; 438 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              456
                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cortex -
                                                                                                                                                                                                                                    0;
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300

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RESULT 5
AAT51747
ID AAT51747
AC AAT5
AC AAT6
AC AAT6
CC AAT7

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                                                                                                                      Query Match
Best Local S
Matches 456
                                                                                                                                                                                                                        An isolated DNA (AAT51747), designated del2.0, comprises a 1988 bp portion of the tobacco RD2 gene (TobRD2) promoter (see also AAT51746), which directs root cortex-specific expression of associated genes: Del2.0 and truncated TobRD2 promoters (see also AAT51748-56) can be used in DNA cassettes to direct the expression c heterologous genes in the root cortex layer of transgenic monocot or dicot plants, e.g. to express Bocillus thuringiensis crystal proteins in tobacco for the control of root-damaging pests. Del2.0 directed high levels of GUS reporter gene expression (4-fold higher than the CaMY35S promoter) in transgenic tobacco root cortex.
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 33-34; 53pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-145698/13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Root cortex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYNC-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Root cortex-specific promoter; TobRD2; tobacco; transgenic plant; insecticide; Bacillus thuringiensis; biological control; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-OCT-1997
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                                                                                                                                                                                              Sequence
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                                                   959
                                                                                                                        456;
                13
                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            cting heterologous gene expression in the root cortex expressing insecticidal Bacillus proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTAGTTGTTATAGGTAAAAAGCAGTTACAGAG
                                                1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATCGGTTCGGTGCGGACGGTTCGATCGGTTTAGTCGATTTTCAAATATTCATTGACACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATTATCGGTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCAGAAGAAACCTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTAATAAAGATACTTGAAATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGA 120
                                                                                 GGAAACATATTCAATACATTGTAGTTTGCTACTCATAATCGCTAGAATACTTTGTGCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specific
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                                                                                                                                                                                            BP; 714 A; 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0508786.
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                                                                                                                                                                                                                                                                                                                                                                                                                           English.
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                                                                                                                      Score 456; DB 18;
Pred. No. 3.8e-68;
Mismatches 0;
                                                                                                                                                                                            302 G;
                                                                                                                                                                                           701 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (del2.0)
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            An isolated DNA (AAT51746) comprises the tobacco RD2 gene (TobRD2) promoter, which directs root cortex-specific specision of associated genes. A clone containing the isolated DNA was obtd. from a tobacco seedling genomic library by screening with TobRD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                       DNA directing heterologous gene expression in the root cortex - used e.g. for expressing insecticidal Bacillus proteins
                                                                                                     Claim 1; Page 32-33;
                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                              Conkling
                                                                                                                                                                                                                                                                                                    28-JUL-1995;
                                                                                                                                                                                                                                                                                                                                    24-JUL-1996;
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                                                                                                     53pp; English.
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Root cortex specific gene TobRD2 promoter
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                                     (first entry)
                                                                                                               DNA;
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Root cortex-specific promoter; TobRD2; tobacco; transgenic plant; insecticide; Bacillus thuringiensis; biological control; ss.
                                          NORTH CAROLINA STATE.
                                                                                   9503-0508786
                                                                                                                       96WO-US12158
                                                                                                                                                                                                                                                                                     /*tag=
2000
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TobRD2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                that TobRD2 mRNA is expressed only in the cortex layer of roots. Truncations of the promoter region (see also AAT51747-54) were prepd. by PCR. The full-length or truncated promoters can be used in DNA cassettes to direct root cortex-specific expression of heterologous genes in transgenic monocot or dicot plants, e.g. to express Bacillus thuringiensis crystal proteins in tobacco for the control of root-damaging pests.
 Conkling MA,
                                                                                                                                                                                                                                                  AAT51751
                                                                                     13-FEB-1997
                                                                                                        WO9705261-A1
                                                                                                                               Nicotiana tabacum
                                                                                                                                                Root cortex-specific promoter; TobRD2; tobacco; transgenic insecticide; Bacillus thuringiensis; biological control; se
                                                                                                                                                                                Root cortex specific gene TobRD2 promoter (del0.7).
                                                                                                                                                                                                        15-OCT-1997
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                                          28-JUL-1995;
                                                               24-JUL-1996;
                      (UYNC-) UNIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                CCTAGTTGTTGTTATAGGTAAAAAGCAGTTACAGAG
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                                                                                                                                                                                                                                                                                                                                                          AATCGGTTCGGTGCGGACGGTTCGATCTGGTTTAGTCGATTTTCAAATATTCATTGACACT
                                                                                                                                                                                                                                                                                                                                                                                                   AATTATCGGTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCAGAAGAAACCTAAA
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                    NORTH CAROLINA STATE
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 Mendu N,
                                           9508-0508786
                                                               96WO-US12158
                                                                                                                                                                                                                                                 DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          702 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.4e-67;
3;
                                                                                                                                                                                                                                                                                                     1414
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ABL32348
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                     01ek
WPI; 2002-130909/17
                                                                                                                                                                                gene;
                                                                                                                                                                                                             Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianemiac; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                              30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
                                                                                                                  03-JAN-2002
                                                                                                                                                                                          acute myeloid leukaemia; Alzheimer's
neurofibromatosis; rheumatoid arthri
                                                                                                                                                                                                                                                                               Human
                                                                                                                                                                                                                                                                                                                                              ABL32348 standard; DNA; 5145 BP
                                                                                             02-JUL-2001; 2001WO-EP07537
                                                                                                                                      WO200200928-A2
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system

associated gene

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arthritis;

psoriasis;

epilepsy; bowel dis

disease;

disease;

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EPIGENOMICS

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Piepenbrock C,

Berlin

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Query Match
Best Local S
Matches 148
                                                                                                                                                                                                                                                                                                                                                                                                                           An isolated DNA (AAT51751), designated del0.7, comprises a 722 bp 5'-deletion mutant of the tobacco RD2 gene (TobRD2) promoter (see also AAT51746), which directs root cortex-specific expression of associated genes. Del0.7 can be used in DNA cassettes to direct the expression of heterologous genes in the root cortex layer of transgenic monocot or dicot plants, e.g. Bacillus thuringiensis crystal proteins in tobacco for the control of root-damaging pests. Del0.7 conferred high levels of GUS reporter gene expression (about twice that of the CaMV35S promoter) in transgenic tobacco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 38; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA directing heterologous gene expression in the root cortex - used e.g. for expressing insecticidal Bacillus proteins
                                                                                                                                                                                                                                                                                                                                                                Sequence 722 BP; 278
                                                                                                                                                                                                                                                                                                                                                                                                           root cortex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1997-145698/13
                                        429
121
                                                                                                                                369
                                                                                                                                                                                                                        309 GTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCAGAAGAAACCTAAAAATCGGTT
                                                                                     61
                                                                                                                                                                                                                                                                        148;
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                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                      GTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCAGAAGAAACCTAAAAATCGGTT
                     TTGTTATAGGTAAAAAAGCAGTTACAGAG 456
                                                                                                                              CGGTGCGGACGGTTCGATCGGTTTAGTCGATTTTCAAATATTCATTGACACTCCTAGTTG
                                                                                   CGGTGCGGACGGTTCGATCGGTTTAGTCGATTTTCAAATATTCATTGACACTCCTAGTTG
                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                           32.5%;
                                                                                                                                                                                                                                                                                                                                                             A; 107 C; 129
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                                                                                                                                                                                                                                                                                           Score 148; I
Pred. No. 1
                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                             G; 208 T;
148
                                                                                                                                                                                                                                                                                           DB 18;
1.5e-16;
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Best Local Similarity
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          07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/uicerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a number of human immune syst genes which are modified by the methylation of cytosines. The can be used in the diagnosis and treatment of immune system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                         cytosine
                                                                                                                                                                                        Human metastasis associated gene SEQ
                                                                                                                                                                                                              26-MAR-2002
                                                                                                                                                                                                                                    ABL34464;
                                                                                                                                                                                                                                                           ABL34464
                                           06-APR-2000;
                                                                                                             W0200177376-A2
                                                                                                                                  Homo sapiens
                                                                 06-APR-2001;
                                                                                         18-OCT-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5145 BP; 1470 A; 27 C; 855 G; 2793 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 321; 32pp +
                                                                                                                                                       is associated methylation;
                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                             TGTTTATATTATGATTTAATTAATTTTTTTTTTTTTAGATATTTAAATTGTTTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTATTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  methylation
                                                                                                                                                                                                                                                                                                                  TTTTGTTTTAAAATATTGTAGTATAAATTTATAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
          2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
                                                                                                                                                                                                              (first entry)
                                                                  2001WO-EP03970
                                           2000DE-1019058
                                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.6%;
                                                                                                                                                       gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    provides a number of human immune system associated
                                                                                                                                                                                                                                                           5145
                                                                                                                                                        cytostatic; ds.
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                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 66.6; DB 24; Pred. No. 0.0053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence Listing;
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                                                                                                                                                                 gene therapy;
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                                                                                                                                                                    cancer;
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RESULT 10
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ID ABL335
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XX Human;
KW Human;
KW antlar
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Best Local
                                                                                                                                                                                   neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease
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                                                                                                                                                                                                                                                                                                            Human; immune system disease; cytosine methylation; antiasthmatic;
antiarteriosclerotic; antianaemic; cytostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful for diagnosis of cancers by also for treatment -
                                                                                                                                                                                                                                                                                                                                                                              Human immune system associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5145 BP; 1470 A; 27 C; 855 G; 2793 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid derived
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                             (first
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                                                                                                                                                                                                                                                                                                                                                                              gene SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159;
                                                                                                                                                                                                                                                                                                                                                                                   1541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5145;
                                                                                                                                                                                          disease;
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid comprising for diagnosis and treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-2000;
01-SEP-2000;
       antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antiporiatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8305 BP; 2181 A; 185 C; 1901 G; 4038 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of human immune system associated system which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, ADDS, epilepsy, neurofibromatosis, theumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EPIG-)
                                                 Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                      Human immune
                                                                                         26-MAR-2002
                                                                                                            ABL33307;
                                                                                                                                ABL33307 standard;
                                                                                                                                                                                                                                                                                                          6304
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                  TATTCAATACATTGTAGTTTGCTACTCATAATCGCTAGAATACTTTGTGCCTTGCTAATA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 1541; 32pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Piepenbrock
                                                                                                                                                                                   GGTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCAGAAGAAACCTAAAAAT 363
                                                                                                                                                                                                                          AAGATACTTGAAATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGAATTAGTA 127
                                                                                                                                                                                                                                            GGTATAGTTCGATATTTTTCAATTTATTATAAAAATAAAAAACTTACCCTAATTATC
                                                                                                                                                                                                                                                                                    ATTTAATGCTTTATTAGTTTTAAACTTACTATATAAATTTTTCATATGTAAAATTTAATC
                                                                                                                                                                                                                                                                                                           TTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCCATGAAAA 187
                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000DE-1032529
2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001WO-EP07537
                                                                   system associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rising fragment of chemically modified treatment of diseases associated with
                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                          14.68;
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                                                                                                                                 6175
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                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 66.4; DB 2
Pred. No. 0.0056;
                                                                   gene SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence Listing; German
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O
                                                                                                                                                                                                                                                                                                                                                                                                                                181;
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abnormal
          anaemia;
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18-JUN-2002 ABK33948; ABK33948

(first entry)

DNA;

ВP

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Query Match
Best Local S
Matches 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01ek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurofibromatosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid comprising frag
for diagnosis and treatment
cytosine methylation -
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6175 BP; 1506 A; 154 C; 1357 G;
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                                                                                                                                                                                                                                                                                                              4675
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4915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                   ATATTCAATACATTGTAGTTTGCTACTCATAATCGCTAGAATACTTTTGTGCCTTGCTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Piepenbrock
ATTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCCATGAAA 186
                                                                                                                                                                                                                                                                                                              AAAGATACTTGAAATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGAATTAGT
                                    CGGTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCA
                                                                            ATTTATTTATGTTTATATTTATTTATTTATTTATATGTATATTTATATTTATATTTAAT
                                                                                                                AATTTAATGCTTTATTAGTTTTAAACTTACTATATAAATTTTTCATATGTAAAATTTAAT
                                                                                                                                                                                                                                   Conservative
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2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rheumatoid arthritis; psoriasis; bowel disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 61; DB 2
Pred. No. 0.046
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 24;
.046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3158 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 6175;
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BP;
4675
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of the printed specification, but format directly from WIPO at

was obtained

'n

electronic

Claim 1; SEQ ID NO 543; 32pp + Sequence Listing; German

The present invention provides a number of human immune system associated

ftp.wipo.int/pub/published_pct_sequences

matrix assisted bisulphite; Human; ds; astrocytoma; DNA for staging of Astrocytomas #16. brain tissue; laser desorption/ionization mass spectrometry.

Homo sapiens.

Human

10-JAN-2002.

02-JUL-2001; 2001WO-EP07538.

30-JUN-2000; 01-SEP-2000; 2000DE-1032529. 2000DE-1043826.

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C, Berlin

Novel chemically modified genomic DNA sequences, useful in the characterisation, classification, differentiation, grading, staging, characterisation, classification, differentiation, grading, staging, treatment and/or diagnosis of astrocytomas or predisposition to

Claim 1; SEQ ID No 31; 37pp; English.

identifying methylation status of one or more cytosine positions, and analysing methylation status of the cytosine positions by reference to one or more data sets. The genomic DNA is chemically treated by using a bisulphite, hydrogen sulphite or disulphite. The amplification or step amplifies DNA which is of particular interest in astrocytoma or brain tissue, based on the specific genomic methylation status of brain tissues, as opposed to background DNA. The amplificates carry a fluorescent label or radionuclide. Optionally, the labels of the amplificates are detachable molecule fragments having a typical mass which are detected in a mass spectrometer. The fragments of chemically pre-treated genomic DNA to be amplified, have a single positive or negative charge for a better detectability in the mass spectrometer. Preferably, the amplificates or fragments of the amplificates are detected by matrix assisted laser descorption/ionization mass spectrometry (MALDI) or using electron spray mass spectrometry (ESI). The present sequence is one of the chemically pre-treated reference DNA camples of the invention complement. Also included are an oil gonuclectide or peptide nucleic primers for (I), probes for detecting cytosine methylation or single-nucleotide swhich hybridises to (I), probes for detecting cytosine methylation or single-nucleotide polymorphisms (SNP) in (I), an array of oilgomers or peptide nucleic acids for analysing diseases associated with the methylation states of the CpG dinucleotides of (I). The array is useful for determining genetic and/or epigenetic parameters, classification, differentiation, grading, staging, treatment and/or diagnosis of astrocytomas, or the predisposition to astrocytomas by analysing cytosine methylations, involves obtaining a biological sample containing genemic DNA, extracting the genomic DNA, converting cytosine bases which are unmethylated at the 5-position, in the genomic DNA sample, to uracil or another base which is dissimilar to cytosine in terms of hybridisation behaviour, by chemical treatment and amplifying chemically pre-treated genomic DNA fragments using the array and a polymerase, where the amplificates carry a detectable label. The method further involves Note: The sequence data for this patent did not form part samples of the invention. or (I) of genomic

Sequence 18997 P 299 C; 4016 G; 10007 T; 0 other;

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Matches
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                                                        Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                             cytosine methylation
                                                                                             WPI; 2002-130909/17.
                                                                                                                     01ek
                                                                                                                                           (EPIG-) EPIGENOMICS AG
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01-SEP-2000;
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                                                                                                                                                                                                                                                      WO200200928-A2
                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                      gene;
                                                                                                                                                                                                                                                                                                                           neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidabetic; antipsoriatic; antinflammatory; cancer; eye disease; arterioscierosis; ana acute myeloid leukaemia; alzheimer's disease; AIDS; epilepsy
                                                                                                                                                                                                                                                                                                                                                                          Human; immune system disease; cytosine methylation;
antiarteriosclerotic; antianaemic; cytostatic; noot
                                                                                                                                                                                                                                                                                                                                                                                                              Human immune
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                                                                                                                                                                                                                                                                                                                   neurofibromatosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13815 GATTTGTTTT 13824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13635 TTTTTTTTTTTTTTTTATATTTTTTTAAAATTTAATATCGTGTTTTTTATTTTAATGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 TTGTAGTTTGCTACTCATAATCGCTAGAATACTTTGTGCCTTGCTAATAAAGATACTTGA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                   Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGATTTATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATTATTAATAGTTTTTTATTTTTTAGATTTTTTTTAGATTTTAAATTGAAATGATAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                    2000DE-1032529
2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                             system associated gene SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                   rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.2%;
                                                                                                                     Berlin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                   psoriasis;
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                                                                                                                                                                                                                                                                                                                                                                                                              543.
                                                                                                                                                                                                                                                                                                                                                                           nootropic,
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                                                                                                                                                                                                                                                                                                                   bowel disease,
                                                                                                                                                                                                                                                                                                                                                                                      antiasthmatic,
                                                         gene, useful
abnormal
                                                                                                                                                                                                                                                                                                                                         anaemia;
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RESULT 14
ABL33576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzhelmer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18997 BP; 4675 A; 299 C; 4016 G; 10007 T; 0 other;
                                                                                                                                                                                                                                                        antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antisoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; ana; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy
                                                                                                                                                                                                                                                                                                               Human; immune system disease; cytosine methylation;
antiarteriosclerotic; antianaemic; cytostatic; nooti
                                                                                                                                                                                                                                                                                                                                                           Human immune
                                                                                                                                                                                                                                                                                                                                                                                                                    ABL33576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL33576 standard; DNA;
          Olek A,
                                                                                                                                        03-JAN-2002
                                                                                                                                                                      WO200200928-A2
                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                              gene;
                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-2002
                                                                    30-JUN-2000;
01-SEP-2000;
                                                                                                             02-JUL-2001;
                                                                                                                                                                                                                                             neurofibromatosis;
                                        (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATTTGTTTT 13824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATTAGTTTTAAACTTACTATATAAATTTTTCATATGTAAAATTTTAATCGGTATAGTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCCATGAAAAATTTAATGCTT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGAATTAGTATTTTGAGTTTA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGATTTATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATATTTTTCAATTTATTATAAAATAAAAACTTACCCTAATTATCGGTACAGTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATTATTAATAGTTTTTTATTTTTTAGATTTTTTTAGATTTTAATTGAAATGATAAG
           Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                               2001WO-EP07537.
                                                                                                                                                                                                                                                                                                                                                          system associated gene SEQ ID NO: 1549
                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                     2000DE-1032529
2000DE-1043826
                                                                                                                                                                                                                                             rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.2%;
                                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                5925
             Berlin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ВP
                                                                                                                                                                                                                                            arthritis;
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                                                                                                                                                                                                                                                                       arteriosclerosis; anaemia;
                                                                                                                                                                                                                                            ease; AIDS; epilepsy;
psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156;
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                                                                                                                                                                                                                                                                                                                                 antiasthmatic;
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RESULT 15 ABL33569

ABL33569 standard; DNA;

8305

ВP

gene;

ds.

30-JUN-2000; 01-SEP-2000;

2000DE-1032529 2000DE-1043826 2001WO-EP07537

02-JUL-2001;

WO200200928-A2 Homo sapiens. antiinflammatory; cancer; eye disease; arteriosclerosis; acute myeloid leukaemia; Alzheimer's disease; AIDS; epile neurofibromatosis; rheumatoid arthritis; psoriasis; bowe

anaemia; disease;

neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; Human immune system associated

gene SEQ ID NO:

26-MAR-2002 ABL33569;

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloscleukaemia, Alzheimer's disease, ADDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 1549; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-130909/17.
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5925 BP; 1510 A; 105 C; 1246 G; 3064 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention provides a number of human immune system associates which are modified by the methylation of cytosines. The sequence be used in the diagnosis and treatment of immune system disorders,
 2439
                                                                      2379
                                                                                                                                                                                                          2259
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                                                                                                                                                                                                                                          125 GTATTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCCATGA
                                                                                                      245
                                  305
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                                                                                                                                                                                                                                                                                                               65
                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                          ATAAAGATACTTGAAATAGCTTAGTTTAAATATATAGCATAATAGATTTTTAGGAATTA 124
                                                                                                                                                                        AAAATTTAATGCTTTATTAGTTTTAAACTTACTATATAAATTTTTCATATGTAAAATTTA
                                                                                                                                                                                                          GAATTTTGAATTTGTTTTTTAGTTTAGGTTTGATATTATATATAGATTTGATTTGTTTTA
                                                                                                                                                                                                                                                                             ATAAGGGATTTTTAGATATAATATTTATATTTAAATTTAAATGTATGTTTTTAAGAATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 methylation
GTATTTTTTGTTGTAGTAAATTAATAAATTTAATGGGTTTT
                                                                                                                                       ATCGGTACAGTTATAGATTTATATAAAAATCTACGGTTCTT
                                                                        ATCGGTATAGTTCGATATTTTTCAATTTATTTTTATAAAATAAAAACTTACCCTAATT
                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                   138;
                                                                                                                                                                                                                                                                                                                                                                                                                      0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     abnormal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acute myeloid
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2318

184 2258

2438

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Best Local Similarity
Matches 171; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheiner's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8305 BP; 2163 A; 185 C; 2060 G; 3897 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 1542; 32pp + Sequence Listing; German.
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                                                                                                                                                                                                                                       2062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188
                                                                                                                                                                        128 TTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCCATGAAAA 187
                                                     308 GGTACAGTTATAGATTTATATAAAATCTACGGTTCTTCAGAAGAAACCTAAAAAT 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 AAGATACTTGAAATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGAATTAGTA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 TATTCAATACATTGTAGTTTGCTACTCATAATCGCTAGAATACTTTGTGCCTTGCTAATA 67
                                                                                                                                                                                                                                    ATTTAATGCTTTATTAGTTTTAAACTTACTATATAAATTTTTCATATGTAAAATTTAATC 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.2%;
nilarity 48.0%;
Conservative
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Pred. No. 0.066;
0; Mismatches 185; Indels
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Search completed: June 9, 2003, 07:16:39
Job time: 192 secs

2, Appli 1, Appli 1, Appli 13, Appl 534, Appl 534, Appli 287, Appli 13, Appli 1186, Appli 1186, Appli 11, Appli

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No. is the number of results predicted by chance to have greater than or equal to the score of the result being posterived by analysis of the total score distribution.
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2003, 07:13:20; Search time 44 Seconds (without alignments) 3178.286 Million cell updates/sec
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US-08-508-786-5
PCT-US96-12158-4
US-08-508-786-3
US-08-508-786-3
PCT-US96-12158-3
US-08-508-786-1
PCT-US96-12158-2
PCT-US96-12158-2
US-08-508-786-6
PCT-US96-12158-1
US-08-508-786-6
PCT-US96-12158-6
US-08-998-416-137
US-08-998-416-137
US-08-998-416-137
US-08-98-416-137
US-08-98-416-138
US-08-98-416-138
US-08-98-416-138
US-08-98-416-138
US-08-98-416-683
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US-08-98-416-683
US-08-98-416-683
US-09-056-075-1
US-09-056-075-3
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Sequence
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                                                                                                               ;; TYPE: nucleic acid
STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (ger
US-08-508-786-5
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US-08-508-786-5
                                                                                                                                                                                 CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051
TELECOMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEPAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1030 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0000000
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                                                        Query Match
Best Local S
Matches 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Conkli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Conkling, Mark A.
APPLICANT: Mendu, Mandini
APPLICANT: Song, Wen
TITLE OF INVENTION: Root Cortex Sp.
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley; Be
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U:
ZIP: 28234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Charlotte
STATE: No. 5837876th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Kenneti
ADDRESSEE: Gibson
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Similarity
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                                                          Conservative
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US-08-446-855A-1
US-08-150-741-1
US-08-487-8268-13
US-08-98-416-837
US-08-998-416-837
US-08-998-416-191
US-08-998-416-191
US-08-947-8268-13
US-08-947-8268-11
US-08-446-855A-1
US-09-150-741-1
US-09-345-882-1
US-09-904-882-1
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2: /cgn2_6/ptodata/1,
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    Query Match
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GENERAL INFORMATION:
                                                                                                                                                                                APPLICATION NUMBER: PCT/US96/
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051
                                                                                                               TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PATENTIN Release #1.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                       TELEPHONE: 919-420-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Mendu, Nar
APPLICANT: Song, Wen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Conkling, Mark A.
                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
ZIP: 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                STREET: Post Off
CITY: Charlotte
STATE: North Car
                                                                              TYPE: nucleic acid
                                                          TOPOLOGY:
                                                                    STRANDEDNESS:
                                                                                                                                                      TELEPHONE:
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                                                                                                                                         919-881-3175
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Length 1030;
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                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPOTED:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/508,786
                                  TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO:
                                                                 CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Root Cortex Specific Gene Promoter NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                           STREET: Post Office Drawer 34
CITY: Charlotte
STATE: No. 5837876th Carolina
                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Gibson
STREET: Post Office Drawer 34009
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Mendu, Nandini
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                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application PC/TUS9612158 GENERAL INFORMATION:
APPLICANT: Conkling, Mark A.
APPLICANT: Mendu, Nandini
APPLICANT: Song, Wen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Sin
Matches 456;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Root Cortex Specific Gene NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                              STATE: N
                                                                                                                                                                                                                                        ADDRESSEE: Kenneth D. Sibley; Bell, ADDRESSEE: Gibson STREET: Post Office Drawer 34009 CITY: Charlotte
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Pred. No. 5.6e-85;
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Best Local Similarity
Matches 456; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Pred. No. 5.6e-85;
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RESULT 5
US-08-508-786-3
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                                                                                                        STREET: FOULTH
CITY: Charlotte
CTATE: No. 5837876th C
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                               APPLICANT: Conkling, Mark A.
APPLICANT: Mendu, Nandini
APPLICANT: Song, Wen
TITLE OF INVENTION: Root Cortex Specific
NUMBER OF SEQUENCES: 9
                                                                                                                                                                            ADDRESSEE: Kenneth
                                                                                               28234
                                                                                                                                                                                                                                                                                                                                    , Application US/08508786 5837876
                                                                                                                                                                  Post Office Drawer 34009
                                                                                                                                                                                                 Kenneth D. Sibley; Bell,
                                                                                                                                  Carolina
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PCT-US96-12158-3
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                                                                                                                                                                                                                      Sequence 3, Application PC/TUS9612158 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 3:
                                                                                                 APPLICANT: Mendu, Nandini
APPLICANT: Song, Wen
TITLE OF INVENTION: Root Cortex Specific Gene
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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LENGTH: 1372 base pairs
TYPE: nucleic acid
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                            ADDRESSEE: Gibson
STREET: Post Office D
CITY: Charlotte
STATE: North Carolina
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REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 50
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                 COUNTRY:
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                                                               Post Office Drawer 34009
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nilarity 100.0%;
Conservative (
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Pred. No. 5.6e-85;
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RESULT 7
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TELEPHONE: 919-420-2200
TELEPAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1372 base pairs
                                                                                             Sequence 2, Application US/08508786 Patent No. 5837876 GENERAL INFORMATION:
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NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
                                              APPLICANT: Conkling, APPLICANT: Mendu, Nai APPLICANT: Song, Wen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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CORRESPONDENCE ADDRESS:
             NUMBER OF SEQUENCES:
                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 100.0%; Score 456; DB 5; Local Similarity 100.0%; Pred. No. 5.6e-85;
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                               RESULT 8
PCT-US96-12158-2
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TELEPHONE: 919-420-2200
TELEPRAY: 919-881-3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1988 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
Sequence 2, Application PC/TUS9612158 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 456;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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Pred. No. 5.8e-85;
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SEQUENCE CHARACTERISTICS:
LENGTH: 1988 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic
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Best Local Similarity
Matches 456; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park &
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TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
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ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 50
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STATE: North Car
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Song, Wen
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Mendu, Nandini
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Pred. No. 5.8e-85;
Pred. No. 5.8e-85;
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NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
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INFORMATION FOR SEQ ID NO: 1:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/508,786
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LENGTH: 2010 base pairs
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MEDIUM TYPE: Floppy
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NUMBER OF SEQUENCES:
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APPLICANT: Mendu,
APPLICANT: Song, V
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AATTATCGGTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCAGAAGAAACCTAAA 1318
                                                              ATGAAAATTTAATGCTTTATTAGTTTTAAACTTACTATATAAATTTTTCATATGTAAAA 1198
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                                                                                                                                                                 ATGAAAAATTTAATGCTTTATTAGTTTTAAACTTACTATATAAATTTTTCATATGTAAAA 240
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VENTION: Root Cortex Specific Gene Promoter
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PCT-US96-12158-1
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APPLICANT: Song, Wen
TITLE OF INVENTION: Root Cortex Specific Gene Promoter
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Sibley, Kenneth D
REGISTRATION NUMBER: 31
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: North Carolina
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                                                                                                                                                                             GCTAATAAAGATACTTGAAATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGA
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                                                ATGAAAAATTTAATGCTTTATTAGTTTTAAACTTACTATATAAATTTTTCATATGTAAAA
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                                                                                                                 ATTAGTATTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCC
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US-08-508-786-6
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                                                                                                                                                                                                     Query Match
                                                                                                                                                                        Matches 148;
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                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 722 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/01
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
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CORRESPONDENCE ADDRESS:
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TOPOLOGY: 11
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                                                                                                                                                                                        Local Similarity
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                                                CGGTGCGGACGGTTCGATCGGTTTAGTCGATTTTCAAATATTCATTGACACTCCTAGTTG 428
                                                                                                              GTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCAGAAGAAACCTAAAAATCGGTT
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Mendu, Nandini
                                                                                                                                                                        Conservative
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                                                                                                                                                                                     32.5%; Score 148; DB 2; 100.0%; Pred. No. 2.6e-22;
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PCT-US96-12158-6
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GENERAL INFORMATION:
                                                                                                             Patent No.
                                                                                                                           Sequence 288,
                                                                                                                                                                                                                                                                                                                                                                                          Matches 148;
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 722 base pairs
                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sibley Kenneth D.
REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
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APPLICANT: Song, Wen
TITLE OF INVENTION: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
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Wendland, Jurgen
Knechtle, Philipp
                                                Pohlmann, Rainer
Steiner, Sabine
                                Mohr, Christine
                                                                                Philippsen,
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SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                309 GTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCAGAAGAAGCCTAAAAATCGGTT
                                                                                                                                 121 TTGTTATAGGTAAAAAGCAGTTACAGAG 148
                                                                                                                                                                                 429 TTGTTATAGGTAAAAAGCAGTTACAGAG 456
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Application US/08998416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.5%; Score 148; DB 5; 100.0%; Pred. No. 2.6e-22;
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Gaps

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RESULT 14
US-09-641-638-651
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   pequence 651, Application US/09641638 Patent No. 6432648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 919-541-8689
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: PAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 168; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                           302
                                                                                                                                                                                                                                                                                                    182 TGAAAAATTTAATGCTTTATTAGTTTTAAACTTACTATATAAATTTTTTCATATGTAAAAT 241
                                                                                                                                                                                                                                                                                                                                                     354
                                                                                                                                                                                                                                                                                                                                                                               124 AGTATTTTGAGTTTAATTACTTATTG--ACTTGTAACAGTTTTTATAATTCCAAGGCCCA 181
                                                                                                                  534 TITATITATITATITAATIAATIAATTA 562
                                                                                                                                                                                                                                                                                                                                                                                                                    4 AACATATTCAATACATTGTAGTTTGCTACTCATAATCGCTAGAATACTTTGTGCCTTGCT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27709
                                                                                                                                                                                                                                                                                                                                                                                                                                            AATAAAGATACTTGAAATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGAATT 123
                                                                                                                                                                                                                                                                                                                                               AAATTAGTTATTAAAATATTATTAGATATTATTATTTTCTTTAATAAATTATTAAATAGA 293
                                                                                                                                                       ATTATCGGTACAGTTATAGATTTATATAA. 330
                                                                                                                                                                                                                             TTAATCGGTATAGTTCGATATTTTTTCAATTTATTTTTATAAAATAAAAAAACTTACCCTA 301
                                                                                                                                                                                                                                                                    TAAATATTATGTTGATTTATATTATTTAATCTTTTTATAAGAATTATTATTAAAAATTAAT
                                                                                                                                                                                         Conservative
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AND USES THEREOF
1152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/998,416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 60.6; DB 4;
Pred. No. 0.00016;
0; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 837;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR PRIOR DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR ETITION NUMBER: US 09/275,267
                                                                                                                                                                                                                                                                                                  NAME/KEY: exon
LOCATION: 12254..12340
OTHER INFORMATION: exon S
NAME/KEY: exon
LOCATION: 12854..13023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM FILE REFERENCE: GENSET. 051CP1
CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US/09/502,330
PRIOR FILING DATE: 2000-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 20
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE:
                                                                                                        LOCATION: 16775..16945
OTHER INFORMATION: exon 13
                                                                                                                                                             LOCATION: 16567..1666/
OTHER INFORMATION: exon
                                                       LOCATION: 17063..17554
OTHER INFORMATION: exon
                                                                                                                                                                                                           NAME/KEY: exon
                                                                                                                                                                                                                         OTHER INFORMATION: exon
                                                                                                                                                                                                                                                                                  OTHER INFORMATION: exon 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens FEATURE:
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                                                                                                                                                                                                                                              NAME/KEY: exon
LOCATION: 1330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 6349..6509
OTHER INFORMATION: exon
                 NAME/KEY: misc_feature
OCATION: 17555..20674
                                                                                                                                                    AME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                      OCATION: 7379..7522
OTHER INFORMATION: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AME/KEY: exon
OCATION: 7379..7522
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LOCATION: 1123..3123
                                                                                                                                                                                                                                                                                                                                                                                              OCATION: 8645..8854
THER INFORMATION: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AME/KEY: exon
OCATION: 3871..4072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AME/KEY: exon
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OCATION: 5552..5633
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OCATION: 3124..3297
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OCATION: 5996..6099
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INFORMATION: 3'regulatory region
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Matches

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NAME/KEY: allele
LCCATION: 6019
OTHER INFORMATION: 10-346-141:
NAME/KEY: allele
LCCATION: 6141
OTHER INFORMATION: 10-346-263:
NAME/KEY: allele
LCCATION: 6183
OTHER INFORMATION: 10-346-305:
NAME/KEY: allele
LCCATION: 6338
OTHER INFORMATION: 10-347-74:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: 10-508-245
NAME/KEY: allele
LOCATION: 1559
OTHER INFORMATION: 10-509-284
NAME/KEY: allele
LOCATION: 1570
                                                                                                                                                                                                                                                                                                      COCATION: 4109
THER INFORMATION: 10-343-278
NAME/KEY: allele
LOCATION: 4170
DTHER INFORMATION: 10-343-339
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AME/KEY: allele
OCATION: 2832
OCATION: 2832
OCATION: 10-513-250
OCATION: 2844
OCATION: 2844
THER INFORMATION: 10-513-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OCATION: 2323
THER INFORMATION: 10-511-337
AME/KEY: allele
OCATION: 2341
THER INFORMATION: 10-512-36 :
AME/KEY: allele
OCATION: 2623
OCATION: 2623
                               AME/KEY: allele
OCATION: 6375
                                                                                                                                                                                                                                                                                                                                                                                                       HER INFORMATION: 10-343-231 : deletion of C
ME/KEY: allele
CATION: 4088
HER INFORMATION: 12-206-366 : polymorphic ba
ME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IER INFORMATION: 10-508-191 : polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATION: 4062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E/KEY: allele
afion: 2947
afion: 10-513-365
EER INFORMATION: 10-513-365
EE/KEY: allele
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E/KEY: allele
ATION: 2048
ER INFORMATION: 10-511-62
                                                                                                                                                                                                                                                                      ATION: 5903
ER INFORMATION: 10-346-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATION: 3802
ER INFORMATION:
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ATION: 2934
ER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /KEY: allele
INFORMATION: 10-347-111 : polymorphic base G or
KEY: allele
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: 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-206-81
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                                                               polymorphic base A or
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231 11244	171 11184	111 11124	11064	51	Query Match Best Local S Matches 153	H 23	~ ⊢ ;	OTHER INFO	NAME/KEY:		`	OTHER INFO	$H \sim$	~ 급	OTHER INFO		LOCATION:	OTHER INFO		LOCATION: OTHER INFO	OTHER INFO	NAME/KEY:	H 2	ئى ج		OTHER INFO	OTHER INFO	NAME/KEY:		Ó
ATATGTAAA AATTTTAAT	TCCAAGGCC AATTTAAAT	GATTTTAGG TTAAAATTA	TTTTTTAAT	TTTGTGCCT	Match 13. Local Similarity 49. hes 153; Conservative		ON: 13524 INFORMATION:		EY: allele	'		e 0		z 			Ž.	INFORMATION:		INFORMATION:		•				INFORMATION:	ION:	EY: allele		
ATTTAATCGG ATTAAATTAA	CATGAAAAAT AAATTTAAAT	AATTAGTATTT	AGCTAAGGAA	TGCTAATAAA	5 8 6		10-507-353	10-507-321	T0-30/-1/0	E 07 - 1 7	10-350-332	10-350-72		10-349-368	10-349-224		10-349-216	10-349-142		10-349-97	10-349-47	,	10-348-391	10-347-348		10-347-271	10-347-220	TO-047 - 200		10-347-165
RATAGTTCGATATTTTTC TTAATTTAATATTAATTT	TTAATGCTTTATTAGTTTT 	TGAGTTTAATTACTTATT 	ATATTTTAATATTTTAA	RATACTTGAAATAGCTTAG	Score 59.4; DB 4; Pred. No. 0.00036; 0; Mismatches 156	,	: polymorphic bas	: polymorphic bas	: porymorphic bas	solumoushin has	: polymorphic bas	: polymorphic base	•	: polymorphic bas	<pre>: polymorphic base</pre>		: deletion of CTG	: polymorphic base		: polymorphic base	: polymorphic base	1 de la companya de l	· polymorphic base	<pre>: polymorphic base</pre>	,	: polymorphic base	: polymorphic base	· horizmorphic soco	100000000000000000000000000000000000000	: polymorphic base
ATATGTAAAATTTAATCGGTATAGTTCGATATTTTTCAATTTATTATAAAATAAAA 2 	TCCAAGGCCCATGAAAAATTTAATGCTTAATTAGTTTAAACTTACTATATAAATTTTTC 2	GATTTTAGGAATTAGTATTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAGT 			Length 20674; ; Indels 0; Gaps		e C or T	e A or C	6	2	e C or T	C OF 1		e C or T	e G or T	•		e G or C	1	A or G	C or T	;	A or a	AorG		A or T	A or G	9	,	Corf
290 11303	230 11243	11183	11123	110	0;																									

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AACTTACCCTAATTATCGGTACAGTTATAGATTTATATAAAAATCTACGGTTCTTCAGAA 350

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; MOLECULE TYPE: L
; ORIGINAL SOURCE:
; ORGANISM: PAG1
US-08-998-416-1137
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US-08-998-416-1137
                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                          Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1137, Application US/08998416 Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 919-541-8689
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 636 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION MADE: CHICAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: CH 0016/97 FILING DATE: 31-DEC-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPLICANT: Wendland, Jurgen
PPLICANT: Knechtle, Philipp
PPLICANT: Rebischung, Corinne
PPLICANT: Rebischung, Corinne
ITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
ITLE OF INVENTION: AND USES THEREOF
JMBER OF SEQUENCES: 1152
JMBER OF SEQUENCES: 1152
JMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NDDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
JIY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGISTRATION NUMBER: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11364 TTAATTTAA 11372
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64 AATAAAGATACTTGAAATAGCTTAGTTTTAAATATAAATAGCATAATAGATTTTAGGAATT 123
                                                                                                             4 AACATATTCAATACATTGTAGTTTGCTACTCATAATCGCTAGAATACTTTGTGCCTTGCT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pohlmann, Rainer
Steiner, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mohr, Christine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Philippsen, Peter
                                                                                                                                                                                                                                                         PAG1692RP
                                                                                                                                                                                                                                                                                         DNA (genomic)
                                                                                                                                                                            12.2%;
                                                                                                                                                                                                                                                                                                                                                                                                               1137 :
                                                                                                                                                        0;
                                                                                                                                                     Score 55.6; DB 4; Length 636; Pred. No. 0.0016; O; Mismatches 134; Indels
                                                                                                                                                     ຸນ
                                                                                                                                                   Gaps
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рь	Ωу	DЪ	Qу	Db	Qy
474 TTTAACTTTAATTTCTTATTATTATTTTTATTATTTAATTAA 517	242 TTAATCGGTATAGTTCGATATTTTTCAATTTATTATAAAA 285	414 TAAATATTATGTTGATTTATATTTATTTAATCTTTTTATAAGAATTATTATTAAAATTAAT 473	182 TGAAAAATTTAATGCTTTATTAGTTTTAAACTTACTATATAAATTTTTTCATATGTAAAAT 241	354 TAAAGATTTAATTTAAATATTGTAAATTATTATTTATTAT	124 AGTATTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCCA 181

Search completed: June 9, 2003, 08:04:35 Job time: 46 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2003, 07:10:45 ; Search time 125 Seconds (without alignments) 5105.512 Million cell updates/sec

Title: Perfect score: US-09-941-042C-1 456

1 ggaaacatattcaatacatt.....ggtaaaaagcagttacagag 456

Scoring table: Gapop 10.0 , Gapext 1.0

Searched:

Total number of hits satisfying chosen parameters:

1740770

870385 seqs, 699768693 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Published_Applications_NA: * /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
1. /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
2. /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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3. /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
3. /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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19	18	17	16	5	14	3	12	11	10	છ	œ	7	6	Ŋ	4	w	N	_	No.
51.2	51.4	51.4	51.6	52	52.2	52.4	52.6	52.8	53	53	53.4	53.4	53.6	53.6	54.4	57	57	58.2	Score
11.2	11.3	11.3	11.3	11.4	11.4	11.5	11.5	11.6	11.6	11.6	11.7	11.7	11.8	11.8	11.9	12.5	12.5	12.8	Query Match
2000	17421	7380	640681	376	3991	4985	3991	11047	15732	6030	272	272	513509	14078	6327	53332	53332	858	Length
9	9	9	10	10	9	9	9	9	9	9	10	10	9	7	9	10	9	9	DB
US-09-938-842A-3652	US-10-239-676-54	US-10-239-676-66	US-09-790-988-1	US-09-960-352-5087	US-10-074-045-60	US-10-094-240-10	US-10-074-045-60	US-10-239-676-187	US-10-239-676-96	US-10-239-676-164	US-09-969-373-608	US-09-969-373-607	US-09-754-853A-4	US-08-781-986A-191	US-10-239-676-151	US-09-801-861-3	US-10-224-562-3	US-10-198-846-7035	ID
Sequence 3652, Ap		-	Sequence 1, Appli	Sequence 5087, Ap		Sequence 10, Appl		Sequence 187, App	~	Sequence 164, App	Sequence 608, App	Sequence 607, App	Sequence 4, Appli	Sequence 191, App	Sequence 151, App	Sequence 3, Appli	Sequence 3, Appli	Sequence 7035, Ap	Description

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4	48 4	48.4	48.6	48.6	48.6	48.6	48.8	48.8	48.8	48.8	49	49	49	49.4	49.4	49.4	49.4	49.6	49.6	49.6	49.6	50	50	50.2	50.4	50.6	
	10 6	10.6	10.7	10.7	10.7	10.7	10.7	10.7	10.7	10.7	10.7	10.7	10.7	10.8	10.8	10.8	10.8	10.9	10.9	10.9	10.9	11.0	11.0	11.0		11.1	
0	30350	12003	12405	8842	7089	714	7038	6815	6306	5979	4187	4187	960	15732	15732	11036	424	335913	335913	437	414	5689	419	7823	640681	9515	
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	TS-10-118-328-3	US-09-764-877-3976	US-10-239-676-36	US-10-239-676-71	US-10-239-676-67	US-10-060-036-256	US-10-239-676-204	US-10-239-676-50	US-10-239-676-223	US-10-239-676-18	US-09-764-855-252	US-10-072-349-252	US-10-198-846-6381	US-10-239-676-96	US-10-239-676-95	US-10-239-676-118	US-10-198-846-2929	US-09-754-853A-3	US-09-754-853A-2	US-09-969-373-937	US-09-960-352-6528	US-10-239-676-90	US-09-960-352-11234	US-10-239-676-197	US-09-790-988-1	US-10-239-676-159	
College of the	Sequence 3. Appli	Sequence 3976, Ap	Sequence 36, Appl	Sequence 71, Appl	Sequence 67, Appl	Sequence 256, App	Sequence 204, App	Sequence 50, Appl	Sequence 223, App	Sequence 18, Appl	Sequence 252, App	Sequence 252, App	Sequence 6381, Ap	Sequence 96, Appl	Sequence 95, Appl	Sequence 118, App	Sequence 2929, Ap	Sequence 3, Appli	Sequence 2, Appli	Sequence 937, App	Sequence 6528, Ap	Sequence 90, Appl	Sequence 11234, A	Sequence 197, App	Sequence 1, Appli	Sequence 159, App	

ALIGNMENTS

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LOCATION:	LOCATION:	LOCATION:	NAME/KEY:	FEATURE:	OTHER IN	LOCATION:	LOCATION:	LOCATION:	LOCATION:	NAME/KEY:	FEATURE:	OTHER IN	LOCATION:	LOCATION:	LOCATION:	LOCATION:	NAME/KEY:	FEATURE:	ORGANISM:	TYPE: DNA	LENGTH: 8	SEQ ID NO	SOFTWARE:	NUMBER OF	PRIOR FILE	PRIOR APPI	CURRENT F	IN	FILE REFE	읁	ဝှု	TITLE OF 1	APPLICANT:	APPLICANT:	APPLICANT:	APPLICANT:	GENERAL INFORMATION:	Publication	Sequence 7035, Application US/10198846	US-10-198-846-7035	RESULT 1
					FORMA		: 506,					FORMA	: 320,				=		: Homo	ם	858	7035	FastSEQ	SEQ	ING	LICAT	ILING	PPLIC	RENCE	INVEN	INVEN	₹					ORMA	No.	35,	5-703	
), 791			c_feat		INFORMATION:	, 565,				•		INFORMATION:), 321,			•	'n						SEQ 1	SEQ ID NOS:	FILING DATE: 2001-07-18	APPLICATION NUMBER: 60/306,220	FILING DATE:	APPLICATION NUMBER:	REFERENCE: MRI-049	INVENTION:	INVENTION:	INVENTION:	Steinmann, Kathleen	Wang, Youzhen	Xu, Yongyao	Lillie, James	TION:	US20	Appli	5/c	
•	5, 739,		_		 				5, 389,			 5	1, 327,			2, 183			sapiens)S: 1	2001	MBE	2: 2	MUN	[-049				nn,	(ouzh	ıgyao	Jame		00500	lcat1		
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	750,				C or		17,		193,			ro or	•	•	•	184,									18	0/30	2002-07-18	US/		Y OF	ENTI	NOVEL GENES,	leen					4A1	01/5		
,86,	763,	σ	١		G	588,	526,	466,	398,			6	349,	281,	237,	185,							Version			6,220	8	10/19		BRE	FICAT								19884		
805,	765,	,899)			599,	527,	488,	399,				350,	294,	238,	186,							on 4.0					US/10/198,846		AST C	TON,	ISOdi							5		
814,	769,	6/2,	3			604,	528,	490,	400,				352,	298,	240,	187,							0	,				σ		BREAST CANCER	FOR IDENTIFICATION, ASSESSMENT	COMPOSITIONS,									
916,	771,	080				607,	529,	497,	408,				355,	304,	241,	188,															SSMEN	, KITS									
, KTB	772,	689,				616,	536,	498,	410,				363,	306,	242,	209,															•	S, AND									
920,	774,	980	9			617,	550,	499,	414,				378,	315,	248,	211,															PREVENTION,					•					
822,	784,	/00,	1			619	557,	501,	434,				379	318,	250,	212,																METHODS									
830,	787,		1						441,					319,	252,	217,	1														AND										

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; TYPE: DNA; ORGANISM: Artificial Sequence; FEATURE: ; FEATURE: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-239-676-151
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US-08-781-986A-191
                                              US-08-781-986A-191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 109; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Publication No. US200 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 151
LENGTH: 6327
 Best Local Similarity
               Query Match
                                                                                                                                     TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO:
                                                                                                                                                         (TTORNEY/AUGUS), BOD
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
WMBER OF SEQUENCES: 5255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORRESPONDENCE ADDRESS:
                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                       LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCCATGAAAAATTTAATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08781986A
o. US20030054436A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 HP Vectra 486/33
                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human
                                                                                                                                                                                                                                                                                                                                                                                                                   Diskette,
                                                                            double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Sciences, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.9%;
11.8%;
                                                                                                                                                                                                                                                                                                                                                                                      MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                          US/08/781,9862
                                                                                                                                                                                                                                                                                                                                                                                                                 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 54.4;
Pred. No. 1
 Score 53.6; DB Pred. No. 3.2;
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                 7;
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               Length 14078;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 4
LENGTH: 513509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/754,853A CURRENT FILING DATE: 2001-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hauge, Brian M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/174,880 PRIOR FILING DATE: 2000-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated Witl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 38-10(15810)B
                                                                                                                                                                                                                                                  LOCATION: (1)..(513509)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: 318013_region_A3
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                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: unsure
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                                                                          136361 TTATGTTTAAAATTTTGAATAAATAATTATTTTGTACGTTCTTTAAAAATTGTAGGGCACT
136301 GTCACAATTTAACACATCATAAAATTAAAAAATATAAATAAATTAAATTGTTTAGATTAAAATT
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                                    182 TGAAAAATTTAATGCTTTATTAGTTTTAAACTTACTATATAAATTTTTCATATGTAAAAT
                                                                                                              122 TTAGTATTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCCA 181
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                                                                                                                                                                                                                                                                                                                                                  (111805)..(113968),(114684)..(115204)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang, Ming Li
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                                                                                                                                                                         Score 53.6; DB Pred. No. 9.1;
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CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT FILING DATE: 2001-10-02
FRIOR APPLICATION NUMBER: US 09/754,853
PRIOR FILING DATE: 2001-01-05
PRIOR PELLING DATE: 2001-01-17
PRIOR EPLLICATION NUMBER: US 09/760,427
PRIOR EPLING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
SEQ ID NO 607
LENGTH: 272
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              CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US 09/754,853
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR FILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR FILING DATE: 2001-05-15
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                                                                                                                                                                                                                                                           Sequence 608, Application US/09969373
Patent No. US20020133852A1
GENERAL INFORMATION:
APPLICANT: Effertz, Roger J.
APPLICANT: Hauge, Brian M.
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Best Local Similarity 50.6%;
Matches 129; Conservative
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TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REFERENCE: 38-10(52679).
                                                                                                                                                                                                  PPLICANT: Hauge, Brian M.
ITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
ILE REFERENCE: 38-10(52679)A
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SEQ ID NOS:
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Pred. No. 1.1;
0; Mismatches 126;
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; LOCATION: (5455)
US-10-239-676-164
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US-10-239-676-164
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                                                                                 Query Match
- rocal Similarity
                                                                               Matches
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SEQ ID NO 164
LENGTH: 6030
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LENGTH: 272
TYPE: DNA
ORGANISM: Glycine max
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APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene
FILE REFERENCE: 5013.1003
CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, C
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                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                               OTHER INFORMATION:
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DE 10019173.8
DE 10032529.7
DE 10043826.1
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                       80 ATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGAATTAGTATTTTGAGTTTTAA 139
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ATTGATTTTTTAATTGTTGTTTTAGTTTTTGAATTAAGAAAATTGAGTTTTAGAATTAT 763
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o. US20030082609A1
                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-04-06
                                                                                                                                                                                                                       chemically treated genomic DNA (Homo sapiens)
                                                                                               11.6%;
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                                                                       Score 53; DB Pred. No. 3.2; O; Mismatches
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Pred. No. 1.1;
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NUMBER OF SEQ ID NOS: 2
SEQ ID NO 96
LENGTH: 15732
TYPE: DNA
                                                                                                                                                                                                         веят Local
Matches 17
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                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBRCCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DE 10019058.8
DE 10019173.8
DE 10032529.7
                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                           2000-04-07
                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1004
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   tch 11.6%;
al Similarity 46.6%;
170; Conservative
                                                                                                                                                                    71 ATACTTGAAATAGCTTAGTTTAAATAGTATAGATATAGATTTTAGGAATTAGTATTT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTAGTTTTAAACTTACTATATAAATTTTTCATATGTAAAATTTAATCGGTATAGTTCGA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCCATGAAAAATTTAATGCTTT
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                                                         TAATGCTTTATTAGTTTTAAACTTACTATATAAATTTTTCATATGTAAAATTTAATCGGT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-04-06
                                                                                                                                                                                                                                                                                       chemically treated genomic DNA (Homo
                                                                                                                                                                                                           ; Score 53; DB 9; Pred. No. 4.2; 0; Mismatches
                                                                                                                                                                                                                            DB 9; Length 15732;
4.2;
                                                                                                                                                                                                              195; Indels
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US-10-239-676-187
Sequence 187, Application US/10239676
Publication No. US20030082609A1
GENERAL INFORMATION:
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SEQ ID NO 187
LENGTH: 11047
TYPE: DNA
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 5013.1003
CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/EP01/03968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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                                                            7887
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                              231
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                 ATATGTAAAATTTAATCGGTATAGTTCGATATTTTTTTTATAAAAT
GTATATGGTATATAATTAGTGGAGAGAAGTGTATTAGAAAGTTTTAATTTAGAAAT
                                                            TTGAATTTTCGTTAGAGATTT-----TTTTTTTTTTTAAAATTTTTTAGAATAGTGTTTG
                                                                                        TCCAAGGCCCATGAAAATTTAATGCTTTATTAGTTTTAAACTTACTATATAAATTTTTC 230
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                                                                                                                                                                                                                                                                                                                                                                                                                    228
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                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                          treated genomic DNA (Homo sapiens)
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RESULT 12
US-10-074-045-60
; Sequence 60, Application US/10074045
; Publication No. US20030092102A1
; GENERAL INFORMATION:

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; LENGTH: 376
; TYPE: DNA
; ORGANISM: Bos taurus
; OGRANISM: Bos taurus
; OGRANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 22-LIB3058-032-Q1-K1-F9

US-09-960-352-5087

Query Match
Best Local Similarity 52.3%; Pred. No. 2.1;
Matches 115; Conservative 0; Mismatches 105; Indels 0; Gaps 0;
Matches 115; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

Matches 115; Conservative 0; Pred. No. 2.1;
Matches 115; Conservative 0; Gaps 0;
Matches 115; Conservative 10;
Mismatches 105; Indels 0; Gaps 0;

Matches 115; Conservative 10;
Mismatches 105; Indels 0; Gaps 0;

Matches 115; Conservative 10;
Mismatches 105; Indels 0; Gaps 0;

Matches 115; Conservative 10;
Mismatches 105; Indels 0; Gaps 0;

Matches 115; Conservative 10;
Mismatches 105; Indels 0; Gaps 0;

Matches 115; Conservative 10;
Mismatches 105; Indels 0; Gaps 0;

Matches 115; Conservative 10;
Mismatches 105; Indels 0; Gaps 0;

Matches 115; Conservative 10;
Mismatches 105; Indels 0; Gaps 0;

Matches 115; Conservative 10;
Mismatches 105; Indels 0; Gaps 0;

Matches 115; Conservative 10;
Mismatches 105; Indels 0; Gaps 0;

Matches 115; Conservative 10;
Mismatches 105; Indels 0; Gaps 0;

Matches 116; Indels 0; Gaps 0;

Matches 116; Indels 10;

Mismatches 105; Indels 0; Gaps 0;

Matches 116; Indels 0; Gaps 0;

Matches 117, Mismatches 105; Indels 0;

Matches 117, Mismatches 10;

Matches 10;
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Post-processing: Minimum Match 0% Maximum Match 100%
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Maximum DB
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Perfect score:
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   7272
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seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   June 9, 2003, 07:10:15; Search time 1128 Seconds (without alignments) 6547.112 Million cell updates/sec
                                                                               Query
Match
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Gapop 10.0 , Gapext 1.0
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em_gss_pro:*
em_gss_rod:*
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AL071206 Drosophil
AL077798 Drosophil
AL071865 Drosophil
AL286627 Tetraodon
AL069706 Drosophil
AL106171 Drosophil
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	CNS015zz	CNS00EO7	BH179465	CNS016CO	CNS00YWL	CNS001FB	CNS02T50		A2550845		H6937	CNS003BD	CNS004ZW	CNS020K7	CNS016LI	CNS00EVL	CNS009G1	CNS07ONJ	вн183498	CNS005XX	CNS00CS1	CNS00ZZU	CNS04D0K	CNS0155H	вн695520	BH460882	CNSOODT7	B0504880	CNS01090	CNSCOLFB	z	CNS015WU	CNS014PQ	×	×	CNS00LT2	CNS014PQ	CNS00DKY
	12	440	BH179465 014_P_10-	AL106578 Drosophil		AL060732 Drosophil		AL300850 Tetraodon		AL059666 Drosophil.	BH693739 BOMGV68TF	AL064091 Drosophil	AL055440 Drosophil	AL175696 Tetraodon	닭	AL069706 Drosophil	AL053529 Drosophil	AL620449 T3 end of	вн183498 023_L_07-		AL059666 Drosophil	AL097152 Drosophil	AL285149 Tetraodon	AL105023 Drosophil	BH695520 BOMNKO6TR	BH460882 BOGFE84TF	AL075293 Drosophil	BO504880 EST612295	ALIO/341 Tetraccon	ALU60/32 Drosophil	AL069440 Drosophil	AL106008 Drosophil		AL103735 Drosophil		AL078714 Drosophil	AL104456 Drosophil	AL071865 Drosophil

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ALIGNMENTS

CNSOOFYG

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Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR32N04 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ALO71206

ALO71206.1 GI:4951245

GSS.

Drosophila melanogaster.

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)

Genoscope.

Direct Submission

ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 CNSOOFYG LOCUS

DEFINITION

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr) - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila nelanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial

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                                                                                                                                                                                                                                                                                                                  JS-10-224-562-3
                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/224,562
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/10224562 Publication No. US20030022229A1 GENERAL INFORMATION:
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Best Local Similarity 41.9
Matches 144; Conservative
                                                                                                                                                                                                                                                   Best Local Similarity Matches 144; Conserv
                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS,
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: CL001098DIV
                                                                                                                                                                                                                                                                                                                          LENGTH: 53332
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 832, 833, 838, 842, 847, 849, 850, 853, 856, OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                  186 AAATTTAATGCTTTATTAGTTTTAAACTTACTATATAAATTTTTCATATGTAAAATTTAA 245
                                                                                                                                            126 TATTTIGAGTITAATTACTTAITIGACTITGTAAACAGTTITTATAATTCCAAGGCCCATGAA 185
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                                                                                                                                                                                                       66 TAAAGATACTTGAAATAGCTTAGTTTAAATAGAATAGCATAATAGATTTTAGGAATTAG 125
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                                                                                                                       TCGGTATAGTTCGATATTTTTTCAATTTATTTTATTAAAAATAAAAAACTTACCCTAATTA 305
                                                            AACCTAAAAATCGGTTCGGTGCGGACGGTTCGATCGGTTTAGTC 396
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ilarity 49.8%;
Conservative
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41.9%;
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Pred. No. 1.2;
0; Mismatches 145; Indels
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Pred. No. 0.23;
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LENGTH: 53332
; TYPE: DNA
; ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                    Sequence 151, Application US/10239676
Publication No. US20030082609A1
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Best Local Similarity 49.8%;
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                                                                                           PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058.8
DE 10019173.8
DE 10032529.7
DE 10043826.1
PRIOR FILING DATE: 2001-04-06
                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
                                                                                                                                                                                                                                                    APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
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TITLE OF INVENTION:
TITLE OF INVENTION:
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CURRENT FILING DATE: 2001-03-09
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                                                         2000-04-06
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SEQ
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                                                                                                                                                                                                                                                                                                               PIEPENBROCK, Christian
ID NOS:
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228
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Pred. No. 1.2;
0; Mismatches 145;
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KEYWORDS
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                                                                TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 AGTATTTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTATAATTCCAAGGCCCATG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 AATAAAGATACTTGAAATAGCTTAGTTTAAATATAAATAGCATAATAGATTTTAGGAATT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed describtion of the library and how to order individual BAC clones, the entire library; or filters for hybridization from the BACPAC Resource Center can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNS04E5M 976 bp DNA linea:
Tetraodon nigroviridis genome survey sequence T7
103P02 of library G from Tetraodon nigroviridis,
                                      Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                        Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Billault, A., Quetier, F., Sauri
                                                                                                                              2 (bases 1 to 976)
Roest-Crollius, H.,
                                                                                                                                                                                              Human gene number estimate provided Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                            Roest-Crollius, H., Jaillon, O., Dasilva, C., Boung
Bernot, A., Fizames, C., Wincker, P., Brottier, P.,
Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                      Acanthomorpha; Acanthopterygil; Percomorpha; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS; genome survey sequence.
Tetraodon nigroviridis.
              Unpublished
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                                                                                        Weissenbach,J
                                                                                                                                                                              Jnpublished
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                                                                                                                                                                                                                                                                                                              (bases 1 to 976)
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/db_xref="taxon:727"
/db_xref="BACR27A24"
/clone="BACR27A24"
/clone_lib="RRCI-98"
/note="end : T7"
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Pred. No. 0.0023;
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                                                                                                        va,C., Fizames,C., Fi
Saurin,W., Bernot,A.
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r,P., Quetier,
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COMMENT

Determination of this BAC-end Sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's

JOURNAL TITLE

> Direct Submission Genoscope.

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                          176 GGCCCATGAAAAATTTTAATGCTTTATTAAACTTATAAACTTATATAAATTTTTCATATG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                         744 WAWATTITUTUWAWATIWIWITWATNATAWIWIAAWIWIATTITITATIATIAAW
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                                                                                                                                                                                                                                                                                                           864 TWWTWTNTTTANAAAWTATATAATWATTTTNTTWAAATTTAATTTTTAAATTAATAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 TAGTATTTTGAGTTTAATTACTTATTGACTTG-----TAACAGTTTTTATAATTCCAA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                624 MMMMNWDAAAAMMMTTTTTTWWWTTTTTWTWTWTTTTNTWTWWDTWWTTTATTTAT 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (12-APR-2000) This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                        fly), ger
AL069706
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                 Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                    Drosophila melanogaster genome sur
BACR29B23 of RPCI-98 library from
                                                                                                   Drosophila melanogaster.
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                                                                                                                                                                      genomic survey sequence.
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/clone_lib="G"
/note="Genoscope s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
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Pred. No. 0.0028;
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g 327
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survey sequence T7 end of BAC:
rom Drosophila melanogaster (fruit
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RESULT 8
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the lacogenic strain 92; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 987)
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) -
                                                                   Submitted (23-JUL-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                                                                                                                                                                                                       GSS.
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                                                                                                                                           Genoscope
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                                                                                                                                                                                                                                                                                                                                                  fly), genomic survey sequence. AL104456
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                                                                                                                     Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCTAGTTGTTGTTAT 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAATCGGTTCGGTGCGGACGGTTCGATCGGTTTAGTCGATTTTCAAATATTCATTGACAC
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/db_xref="taxon:7227"
/db_cref="taxon:7227"
/clone="BACR27A24"
/clone_lib="RPCI-98"
/note="end : T7"
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Pred. No. 0.0036;
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Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and
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Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR48P19 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                      Direct Submission
Submitted (11-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
/clone="BARON12P22"
/clone_11b="DrosBAC"
/plasmid="bBeloBAC11"
/note="end : SP6"
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31.7%;
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                  Pterygota;
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Mammoser in Pieter de Jong's laboratory in

the

Department

of.

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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 60
LENGTH: 3991
TYPE: DNA
ORGANISM: Homo sapiens
US-10-074-045-60
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                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 10
                                                                                                                                      Matches
                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/094,240
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 10/056,405
PRIOR FILING DATE: 2002-01-24
                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/264,649 PRIOR FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ZWIEBEL, LAURENCE J.
TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF
FILE REFERENCE: N8289
                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: PTZ21C1
CURRENT APPLICATION NUMBER: US/10/074,045
CURRENT FILING DATE: 2002-02-14
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                   LENGTH: 4985
TYPE: DNA
ORGANISM: Anopheles
                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocal Similarity
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3226
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                                                                                                                                      140;
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                                                                                              TCATAATCGCTAGAATACTTTGTGCCTTGCTAATAAAGATACTTGAAATAGCTTAGTTTA 92
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                                                                TTATAGATTTATATAAAAATCTACGGTTCTTCAGA 349
                               AATATAAATAGCATAATAGATTTTAGGAATTAGTATTTTGAGTTTAATTACTTATTGACT 152
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Pred. No. 3.
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Pred. No. 3.3;
                                                                                                                                  Mismatches 146;
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                                                                                                                                                                  DB 9;
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-074-045-60
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Best Local Similarity 52.5%;
Matches 137; Conservative
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NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 60
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                           APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ21C1
NUMBER OF SEQ ID NOS:
EQ ID NO 5087
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Pred. No. 3.
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RESULT 12
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                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                      AUTHORS
                                                                               source
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                                                                                                                                                                                                                                                                           Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 987)
                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN12P22 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL104456
                                                                                                                             Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNS014PQ
                                                                                                                                                                                                                               Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fj
                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                      Genoscope
                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                 AL104456.1 GI:5616067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAA 362
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                                                                                                                     Genevieve Payan. It has been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:7227"
/clone="BACN11G11"
        /plasmid="pBeloBAC11"
                        /clone="BACN12P22"
/clone_lib="DrosBAC"
                                                  /organism="Drosophila
/db_xref="taxon:7227"
                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.2%;
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SP6"
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                                                                 melanogaster*
                                                                                                                     constructed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA
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                                                                                                                                                                                                          - Web : www.genosope.cns.fr)
- Web : www.genosope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a Collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton project grant. The DNA was prepared from embryos by Alain Bucheton
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Drosophile melanogaster genome sure BACN15E10 of DrosBAC library from a flux, genomic survey sequence.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musco
Ephydroidea; Drosophilidae; Drosophila.

[ bases 1 to 1203)
                                                                                                                                                                                                                                                                                                                                                                                      Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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/clone="BACN15E10"
/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
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                                                                                                      /organism="Drosophila
/db_xref="taxon:7227"
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Muscomorpha;
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and of BAC
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RESULT 14
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                                                                                                                                                                                                                                                        Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo. NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain y2; cn bw sp. the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1116
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR29P01 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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                                                                                                                                                                                                                                          at http://bacpac.med.buffalo.edu/drosophila_bac.htm
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                                                                                                                              /organism="Drosophila
/db_xref="taxon:7227"
/clone="BACR29P01"
                                                              /clone_lib="RPCI-98"
/note="end : TET3"
66 c 104 g
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Matches 128; Conservative
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Genoscope

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fi
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                                                                                                                                                                                                                                                    and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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/clone_lib="RPCI-98"
/note="end : TET3"
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62 937	3 AAACATATICAATACATTGTAGTTTGCTACTATAATCGCTAGAATACTTTGTGCCTTGC 62 :	990	g Q
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BP 191 yavo by a consider of the Bosynth of the Bosynth of the Bosynth of the Bacternination of this BAC-end sequence was carried out as part of the Collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruittly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Canadian and Canadian at the Roswell Park Canadian Institute in Buffalo,
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                          Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster genome survey sequence BACR17N06 of RPCI-98 library from Drosophila
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AL077798
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/db_xref="taxon:7227"
/clone="BACR32N04"
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Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part collaboration with the Berkeley Drosophila Genome Project (BDGP)
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammoser in Pieter de Jong's laboratory in the Department
                                                                                                                                                                                                                                                                               Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNSOODKY 928 bp DNA linear GSS 04-JUN-19
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR27A24 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NY. The library is named RPCI-98 and was constructed by partial Eccorl digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                          Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                     Genoscope.
Direct Submission
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AL071865
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/db_xref="taxon:7227"
/clone="BACR17N06"
/clone_lib="RPCI-98"
/note="end: T7"
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RESULT 6
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                                                                                                                                                                                                                                                                              CNS0161D 1225 bp DNA linear GSS 26-JUL-19
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN15C18 of DrosBAC library from Drosophila melanogaster (fruit
   Determination collaboration
                                            Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr
                                                                                                                Neoptera; Endopterygota; Diptera; Brachycera; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1225)
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Drosophila melanogaster
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                                                                                Direct Submission
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 Web : www.genoscope.cns.fr)
stermination of this BAC-end sequence was
bilaboration with the European Drosophila
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/db_xref-"taxon:7227"
/clone-Taxon:7227"
/clone_Lib-"RPCI-98"
/note-"end : T7"
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Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part collaboration with the Berkeley Drosophila Genome Project (BDGI The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org.separed by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department
                                                                                                                                                                                                                          Drosophila melanogaster.
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Inse
Neoptera, Endopterygota, Diptera, Brachycera,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster genome survey sequence T7 end of BAC # BACR27A24 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                       Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fi
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Direct Submission
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/note="end : SP6"
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/clone_lib="DrosBAC"
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/db_xref="taxon:7227"
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TITLE
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Best Local :
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127; Conserv
                                                                                                                                        Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN16D22 of DrosBAC library from Drosophila melanogaster (f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and how to order individual BAC clones, the entire library, of filters for hybridization from the BACPAC Resource Center can found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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    Web: www.genoscope.cns.fr)
    Determination of this BAC-end sequence was collaboration with the European Drosophila

                                                          Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fi
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AL106896.1
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/db_xref="taxon:7227"
/clone="BACR48P19"
/clone_lib="RPCI-98"
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                                                          d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                  - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster genome survey sequence T7 end of BAC BACN11G11 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                    Submitted (23-JUL-1999) Genoscope
BP 191 91006 EVRY cedex - FRANCE (E-
                                                                                                                                                                                                                                                              Genoscope.
Direct Submission
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Neoptera; Endopterygota; Diptera; Brachycera; Muscc Ephydroidea; Drosophilidae; Drosophila
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